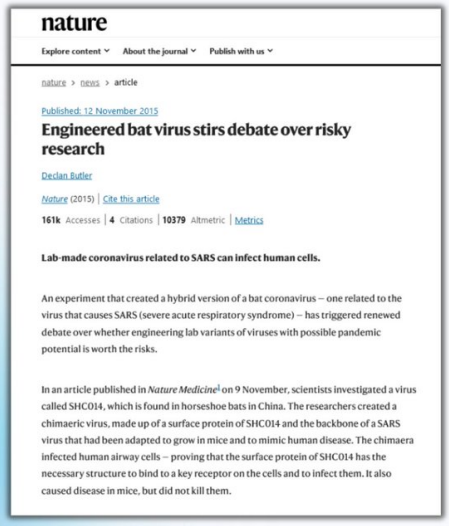
Destiny Rezendes @dezzie_rezzie

Nov 18, 2023 • 17 tweets • dezzie_rezzie/status/1725755860939333659

1🧵In the early months of 2020 there were many people who knew something was off about the prescribed narrative. Critics were quick to point out all the holes in the official story & one article kept resurfacing, "Engineered Bat Virus Stirs Debate Over Risky Research."

2🧵The infamous article published in Nature by Declan Butler, Nov. 12th 2015 wasn't the actual research but was a critical overview of the GoF research conducted by Ralph Baric on Coronaviruses. Baric's work was published just 3 days earlier & caused immediate concern.



nature

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Published: 12 November 2015

Engineered bat virus stirs debate over risky research

Declan Butler

Nature (2015) | Cite this article

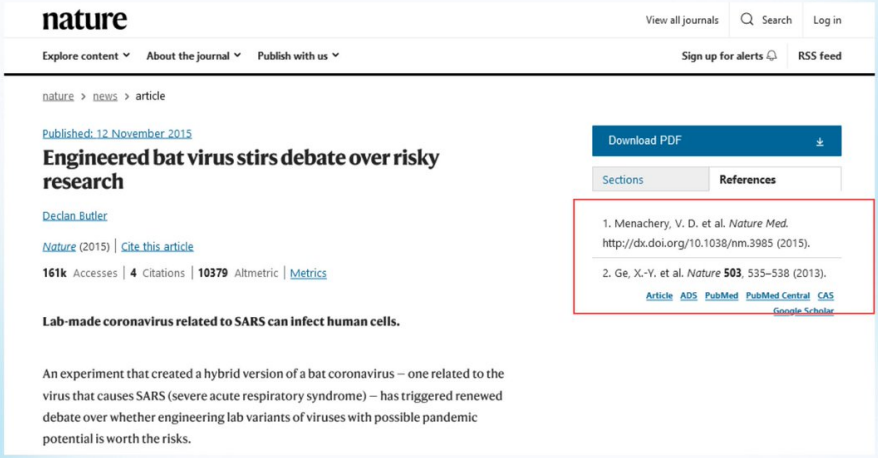
161k Accesses | **4** Citations | **10379** Altmetric | Metrics

Lab-made coronavirus related to SARS can infect human cells.

An experiment that created a hybrid version of a bat coronavirus – one related to the virus that causes SARS (severe acute respiratory syndrome) – has triggered renewed debate over whether engineering lab variants of viruses with possible pandemic potential is worth the risks.

In an article published in *Nature Medicine*[1] on 9 November, scientists investigated a virus called SHC014, which is found in horseshoe bats in China. The researchers created a chimaeric virus, made up of a surface protein of SHC014 and the backbone of a SARS virus that had been adapted to grow in mice and to mimic human disease. The chimaera infected human airway cells – proving that the surface protein of SHC014 has the necessary structure to bind to a key receptor on the cells and to infect them. It also caused disease in mice, but did not kill them.

source: https://www.nature.com/articles/nature.2015.18787



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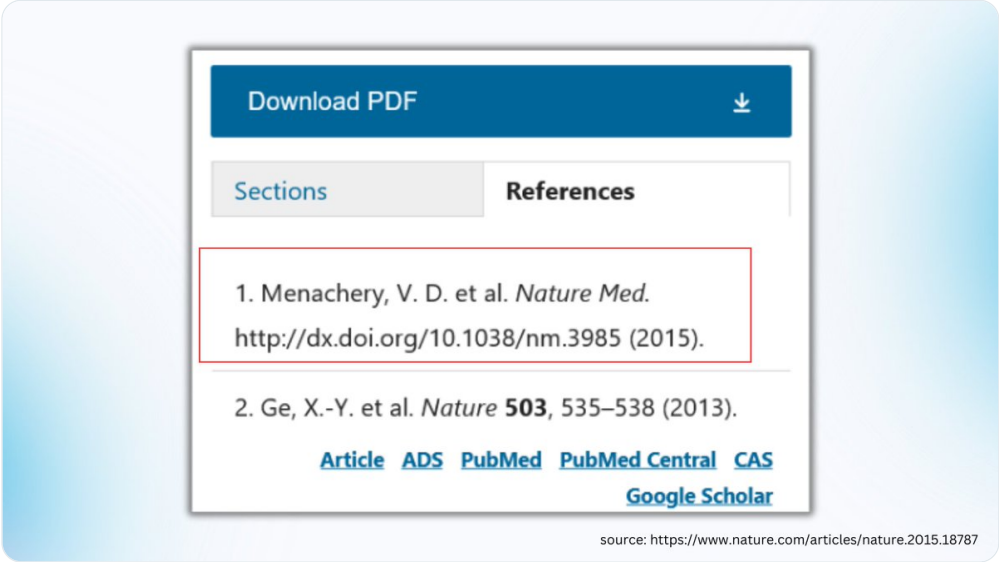
Sections | References

1. Menachery, V. D. et al. *Nature Med.* http://dx.doi.org/10.1038/nm.3985 (2015).

2. Ge, X.-Y. et al. *Nature* **503**, 535–538 (2013).

Article ADS PubMed PubMed Central CAS Google Scholar

source: https://www.nature.com/articles/nature.2015.18787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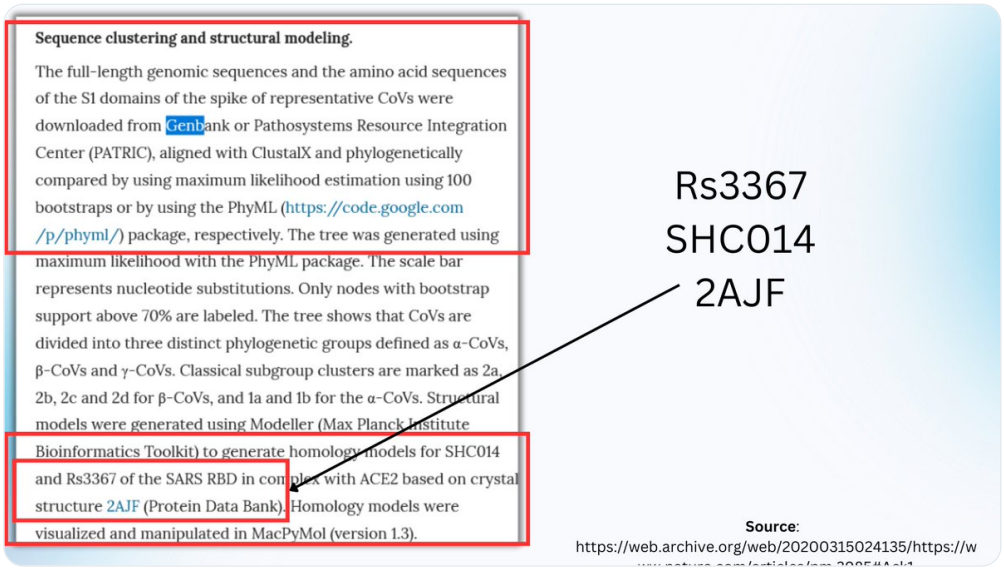
Sections
References
1. Menachery, V. D. et al. Nature Med. http://dx.doi.org/10.1038/nm.3985 (2015).
2. Ge, X.-Y. et al. Nature 503, 535–538 (2013).
Article ADS PubMed PubMed Central CAS
Google Scholar
source: https://www.nature.com/articles/nature.2015.18787

3 Butler cites Baric's research, "A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence." Most of us are familiar w/ this paper as it's been cited as proof of GoF work with WIV of CoVs. But do you know which version matters? Yes, "Which?"

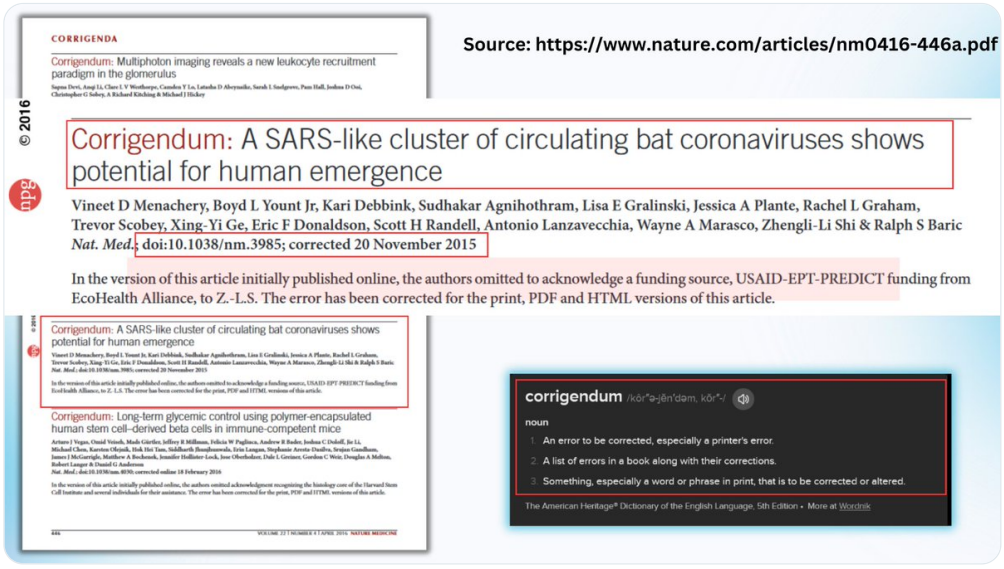
Source: https://web.archive.org/web/20200315024135/https://www.nature.com/articles/nm.3985#Ack1

Source: https://web.archive.org/web/20200315024135/https://www.nature.com/articles/nm.3985#Ack1

MENU
nature medicine
Letter | Published: 09 November 2015
A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence
Vineet D Menachery , Boyd L Yount Jr, Kari Debbink, Sudhakar Agnihothram, Lisa E Gralinski, Jessica A Plante, Rachel L Graham, Trevor Scobey, Xing-Yi Ge, Eric F Donaldson, Scott H Randell, Antonio Lanzavecchia, Wayne A Marasco, Zhengli-Li Shi & Ralph S Baric
Nature Medicine 21, 1508–1513(2015) | Cite this article
835k Accesses | 93 Citations | 4190 Altmetric | Metrics
A Corrigendum to this article was published on 06 April 2016
This article has been updated
Abstract
The emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. Here we examine the disease potential of a SARS-like virus, SHC014-CoV, which is currently circulating in Chinese horseshoe bat populations[1]. Using the SARS-
About this article
Cite this article
Menachery, V., Yount, B., Debbink, K. et al. A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. Nat Med 21, 1508–1513 (2015). https://doi.org/10.1038/nm.3985
Download citation
Received 12 June 2015
Accepted 08 October 2015
Published 09 November 2015
Issue Date December 2015
DOI https://doi.org/10.1038/nm.3985
Acknowledgements
Research in this manuscript was supported by grants from the National Institute of Allergy & Infectious Disease and the National Institute of Aging of the US National Institutes of Health (NIH) under awards U19AI109761 (R.S.B.), U19AI107810 (R.S.B.), AI085524 (W.A.M.), F32AI102561 (V.D.M.) and K99AG049092 (V.D.M.), and by the National Natural Science Foundation of China awards 81290341 (Z.-L.S.) and 31470260 (X.-Y.G.), and by USAID-EPT-PREDICT funding from EcoHealth Alliance (Z.-L.S.). Human airway epithelial cultures were supported by the National Institute of Diabetes and Digestive and Kidney Disease of the NIH under award NIH DK065988 (S.H.R.). We also thank M.T. Ferris (Dept. of Genetics, University of North Carolina) for the reviewing of statistical approaches and C.T. Tseng (Dept. of Microbiology and Immunology, University of Texas Medical Branch) for providing Calu-3 cells. Experiments with the full-length and chimeric SHC014 recombinant viruses were initiated and performed before the GOF research funding pause and have since been reviewed and approved for continued study by the NIH. The content is solely the responsibility of the authors and does not necessarily represent the official views of the NIH.


Sequence clustering and structural modeling.
The full-length genomic sequences and the amino acid sequences of the S1 domains of the spike of representative CoVs were downloaded from Genbank or Pathosystems Resource Integration Center (PATRIC), aligned with ClustalX and phylogenetically compared by using maximum likelihood estimation using 100 bootstraps or by using the PhyML (https://code.google.com/p/phyml/) package, respectively. The tree was generated using maximum likelihood with the PhyML package. The scale bar represents nucleotide substitutions. Only nodes with bootstrap support above 70% are labeled. The tree shows that CoVs are divided into three distinct phylogenetic groups defined as α-CoVs, β-CoVs and γ-CoVs. Classical subgroup clusters are marked as 2a, 2b, 2c and 2d for β-CoVs, and 1a and 1b for the α-CoVs. Structural models were generated using Modeller (Max Planck Institute Bioinformatics Toolkit) to generate homology models for SHC014 and Rs3367 of the SARS RBD in complex with ACE2 based on crystal structure 2AJF (Protein Data Bank). Homology models were visualized and manipulated in MacPyMol (version 1.3).
Rs3367
SHC014
2AJF
Source:
https://web.archive.org/web/20200315024135/https://w

4🧵 There are actually 3 versions. The original Nov 2015. The second version is the Corrected Version of 2016. The 2016 version was to correct missing information, namely to acknowledge the NIH gave funding to EHA thru USAID TO Zhengli-Shi.


CORRIGENDA
Corrigendum: Multiphoton imaging reveals a new leukocyte recruitment paradigm in the glomerulus
Source: https://www.nature.com/articles/nm0416-446a.pdf
© 2016
Corrigendum: A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence
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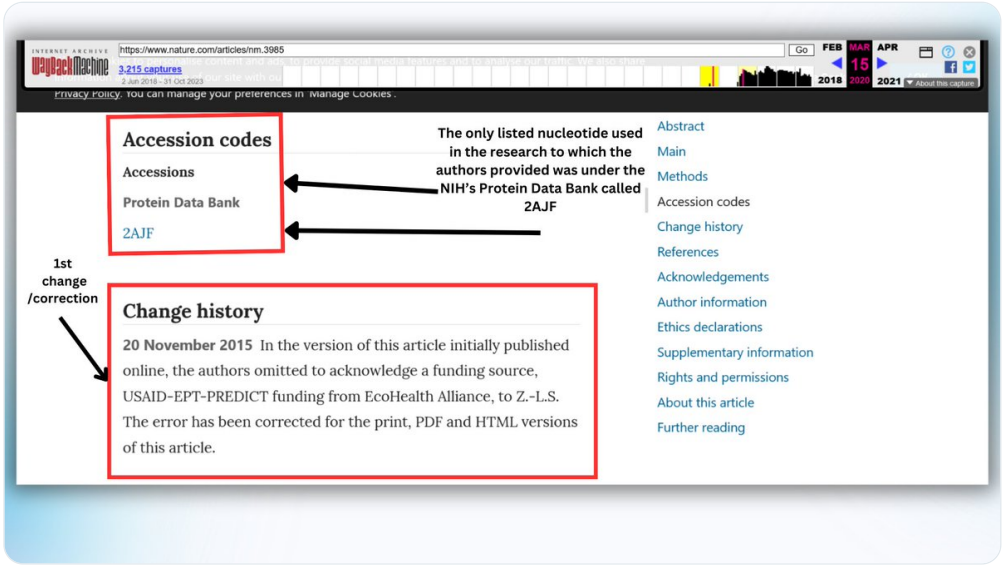
Nat. Med.; doi:10.1038/nm.3985; corrected 20 November 2015
In the version of this article initially published online, the authors omitted to acknowledge a funding source, USAID-EPT-PREDICT funding from EcoHealth Alliance, to Z.-L.S. The error has been corrected for the print, PDF and HTML versions of this article.
Corrigendum: Long-term glycemic control using polymer-encapsulated human stem cell–derived beta cells in immune-competent mice
corrigendum /kôr"ə-jĕn'dəm, kŏr"-/
noun
1. An error to be corrected, especially a printer's error.
2. A list of errors in a book along with their corrections.
3. Something, especially a word or phrase in print, that is to be corrected or altered.
The American Heritage® Dictionary of the English Language, 5th Edition • More at Wordnik


https://www.nature.com/articles/nm.3985
3,215 captures
Accession codes
Accessions
Protein Data Bank
2AJF
The only listed nucleotide used in the research to which the authors provided was under the NIH's Protein Data Bank called 2AJF
1st change /correction
Change history
20 November 2015 In the version of this article initially published online, the authors omitted to acknowledge a funding source, USAID-EPT-PREDICT funding from EcoHealth Alliance, to Z.-L.S. The error has been corrected for the print, PDF and HTML versions of this article.
Abstract
Main
Methods
Accession codes
Change history
References
Acknowledgements
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Ethics declarations
Supplementary information
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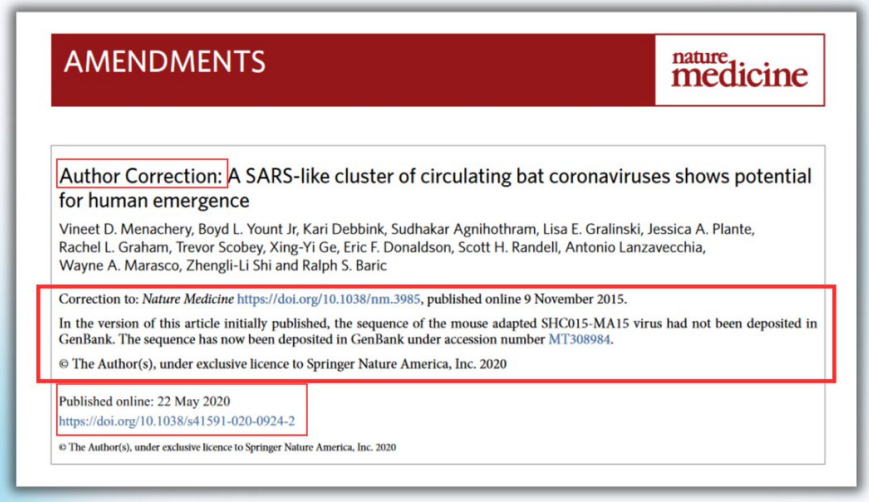
Further reading

5🧵 The third time the landmark paper was changed occurred on May 22nd 2020. That's 4yrs, 6 mos & 14 days post publication! Was is a small error? NO! Turns out the chimeric CoV they cooked was NEVER uploaded to Genbank! The genome of the lab made virus wasn't documented properly!



AMENDMENTS

nature medicine

Author Correction: A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

Vineet D. Menachery, Boyd L. Yount Jr, Kari Debbink, Sudhakar Agnihothram, Lisa E. Gralinski, Jessica A. Plante, Rachel L. Graham, Trevor Scobey, Xing-Yi Ge, Eric F. Donaldson, Scott H. Randell, Antonio Lanzavecchia, Wayne A. Marasco, Zhengli-Li Shi and Ralph S. Baric

Correction to: *Nature Medicine* https://doi.org/10.1038/nm.3985, published online 9 November 2015.

In the version of this article initially published, the sequence of the mouse adapted SHC015-MA15 virus had not been deposited in GenBank. The sequence has now been deposited in GenBank under accession number MT308984.

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Published online: 22 May 2020
https://doi.org/10.1038/s41591-020-0924-2

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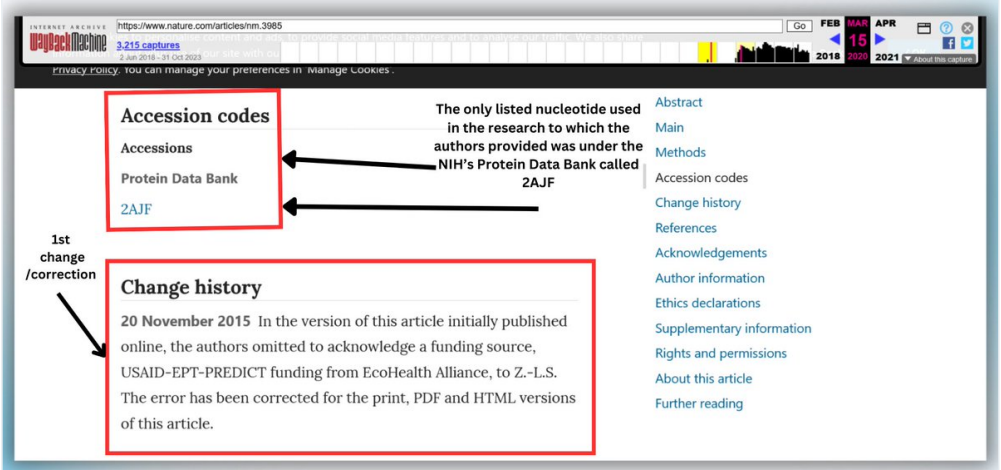
LINK: https://ratical.org/PandemicParallaxView/SARS-like-cluster-coronarius-2015.pdf



https://www.nature.com/articles/nm.3985

3,215 captures

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Accession codes

Accessions

Protein Data Bank

2AJF

The only listed nucleotide used in the research to which the authors provided was under the NIH's Protein Data Bank called 2AJF

1st change /correction

Change history

20 November 2015 In the version of this article initially published online, the authors omitted to acknowledge a funding source, USAID-EPT-PREDICT funding from EcoHealth Alliance, to Z.-L.S. The error has been corrected for the print, PDF and HTML versions of this article.

Abstract
Main
Methods
Accession codes
Change history
References
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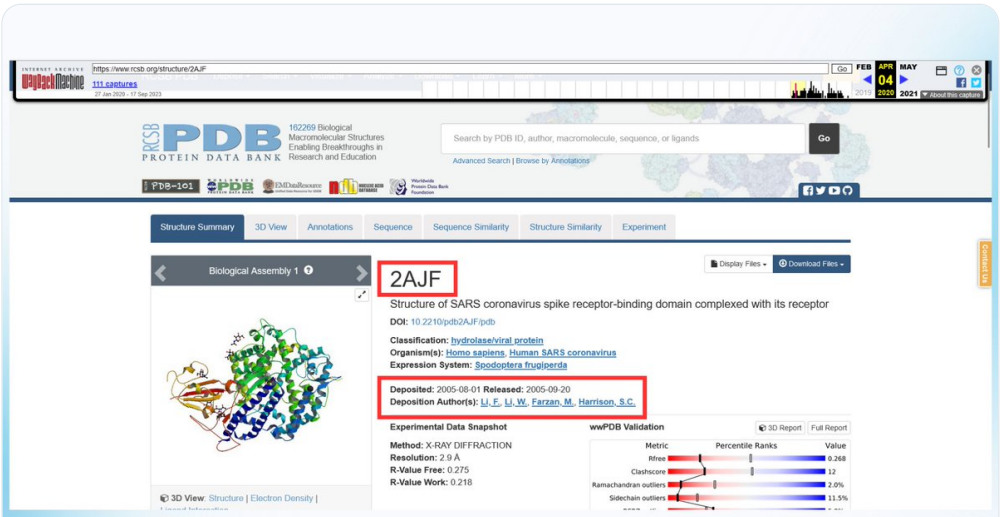
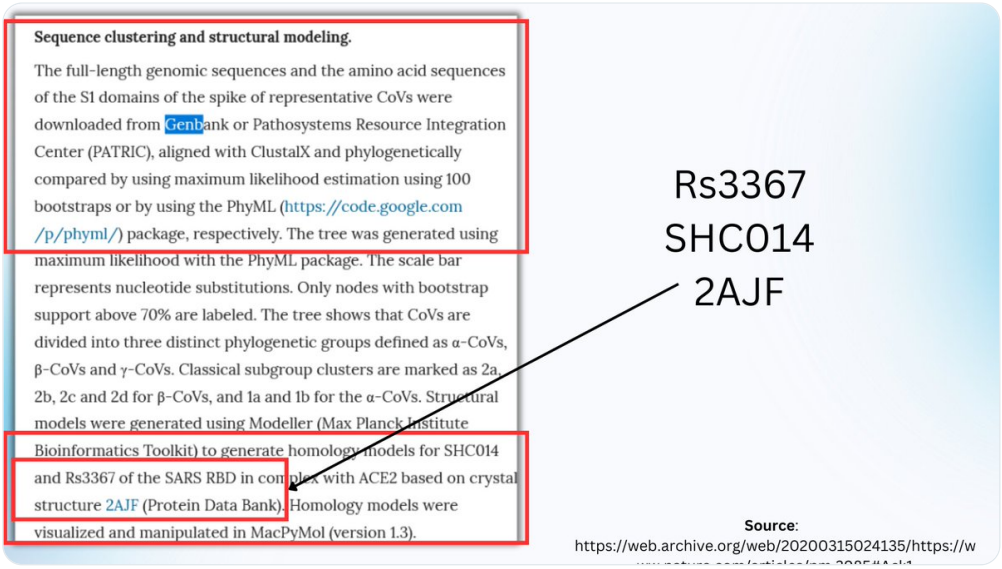
Further reading



Link: https://web.archive.org/web/20200404233128/https://www.rcsb.org/structure/2AJF#carousel-structuregallery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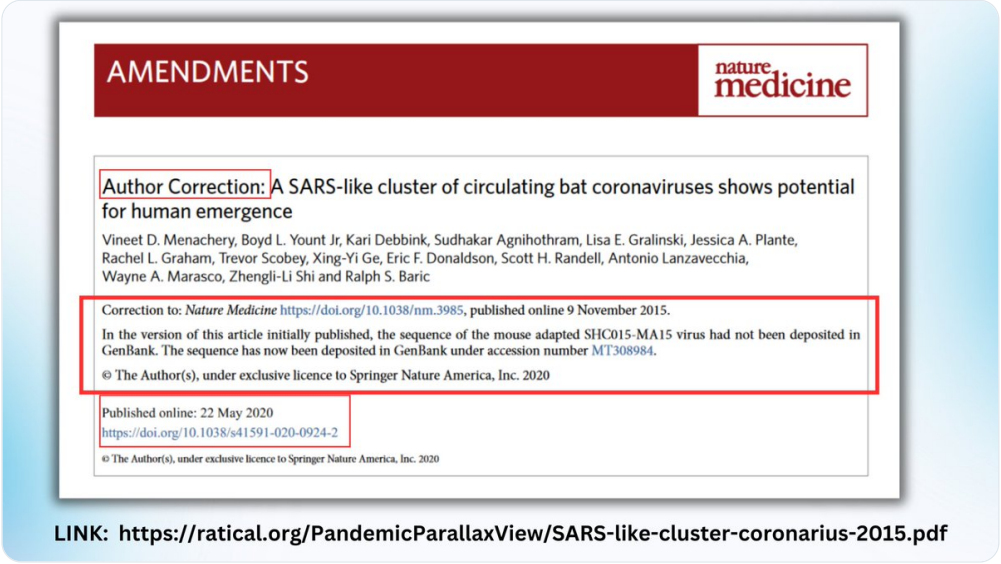
Rs3367
SHC014
2AJF
Source:
https://web.archive.org/web/20200315024135/https://w

6 So, not only did they try to disassociate themselves from USAID Predict Prevent and its ties with EHA, but they RISK GOF research making CoV's during a moratorium was never sequenced and published on Genbank?! Not til 2 & 1/2 months AFTER the C19 pandemic was announced!



AMENDMENTS

nature medicine

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Published online: 22 May 2020
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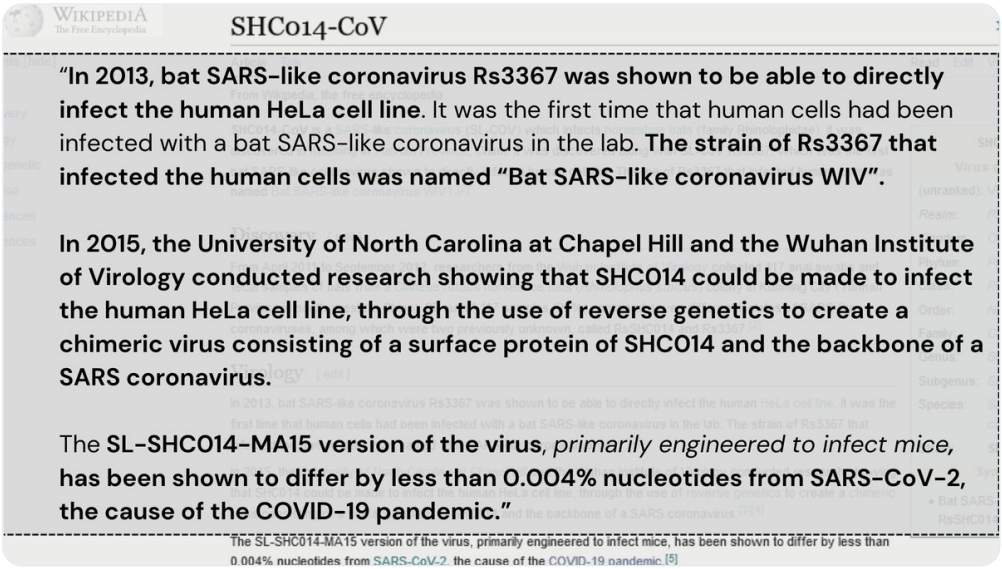
LINK: https://ratical.org/PandemicParallaxView/SARS-like-cluster-coronarius-2015.pdf

7 Keep in mind what Wikipedia currently has to say about that chimeric virus [SHC014]from Baric's work: SHC015 "...has been shown to differ by less than 0.004% nucleotides from SARS-CoV-2 the cause of the Covid-19 pandemic"



WIKIPEDIA The Free Encyclopedia

SHC014-CoV

"In 2013, bat SARS-like coronavirus Rs3367 was shown to be able to directly infect the human HeLa cell line. It was the first time that human cells had been infected with a bat SARS-like coronavirus in the lab. **The strain of Rs3367 that infected the human cells was named "Bat SARS-like coronavirus WIV".**

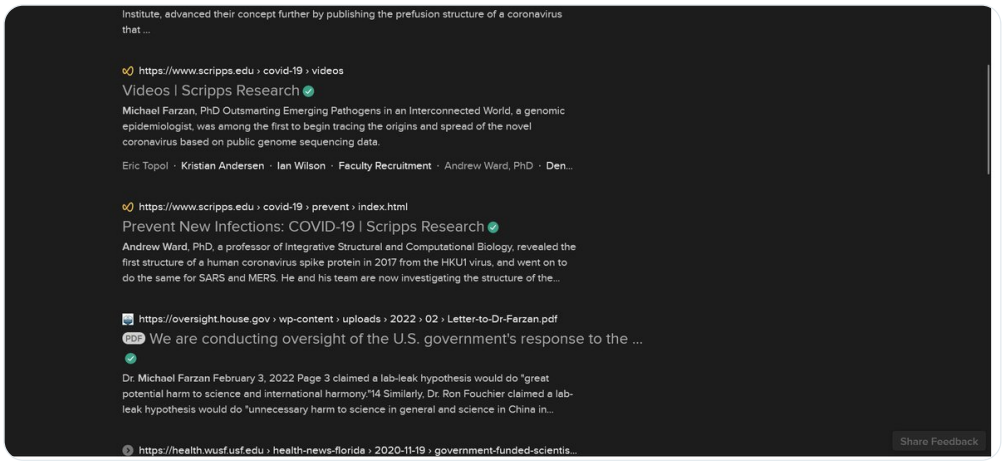
In 2015, the University of North Carolina at Chapel Hill and the Wuhan Institute of Virology conducted research showing that SHC014 could be made to infect the human HeLa cell line, through the use of reverse genetics to create a chimeric virus consisting of a surface protein of SHC014 and the backbone of a SARS coronavirus.

The **SL-SHC014-MA15 version of the virus**, *primarily engineered to infect mice*, **has been shown to differ by less than 0.004% nucleotides from SARS-CoV-2, the cause of the COVID-19 pandemic."**

The SL-SHC014-MA15 version of the virus, primarily engineered to infect mice, has been shown to differ by less than 0.004% nucleotides from SARS-CoV-2, the cause of the COVID-19 pandemic.[5]

8 What's more is the only protein cited in the original work was 2JAF along with the backbones of Rs3367 and SHC014. 2AFJ links back to 4 Harvard doctors [2005]on whom worked at Scripps, Michael Farzan.

HUMAN VACCINES PROJECT
The Global COVID Lab Meeting
"ACE2, the SARS-CoV-2 S protein, and better RBD-based vaccines"
Michael Farzan, Ph.D.
Chair and Professor
Department of Immunology and Microbiology
The Scripps Research Institute


Institute, advanced their concept further by publishing the prefusion structure of a coronavirus that ...
https://www.scripps.edu › covid-19 › videos
Videos | Scripps Research
Michael Farzan, PhD Outsmarting Emerging Pathogens in an Interconnected World, a genomic epidemiologist, was among the first to begin tracing the origins and spread of the novel coronavirus based on public genome sequencing data.
Eric Topol · Kristian Andersen · Ian Wilson · Faculty Recruitment · Andrew Ward, PhD · Den...
https://www.scripps.edu › covid-19 › prevent › index.html
Prevent New Infections: COVID-19 | Scripps Research
Andrew Ward, PhD, a professor of Integrative Structurel and Computational Biology, revealed the first structure of a human coronavirus spike protein in 2017 from the HKU1 virus, and went on to do the same for SARS and MERS. He and his team are now investigating the structure of the...
https://oversight.house.gov › wp-content › uploads › 2022 › 02 › Letter-to-Dr-Farzan.pdf
PDF We are conducting oversight of the U.S. government's response to the ...
Dr. Michael Farzan February 3, 2022 Page 3 claimed a lab-leak hypothesis would do "great potential harm to science and international harmony."14 Similarly, Dr. Ron Fouchier claimed a lab-leak hypothesis would do "unnecessary harm to science in general and science in China in...
https://health.wusf.usf.edu › health-news-florida › 2020-11-19 › government-funded-scientis...
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Scripps Research Institute

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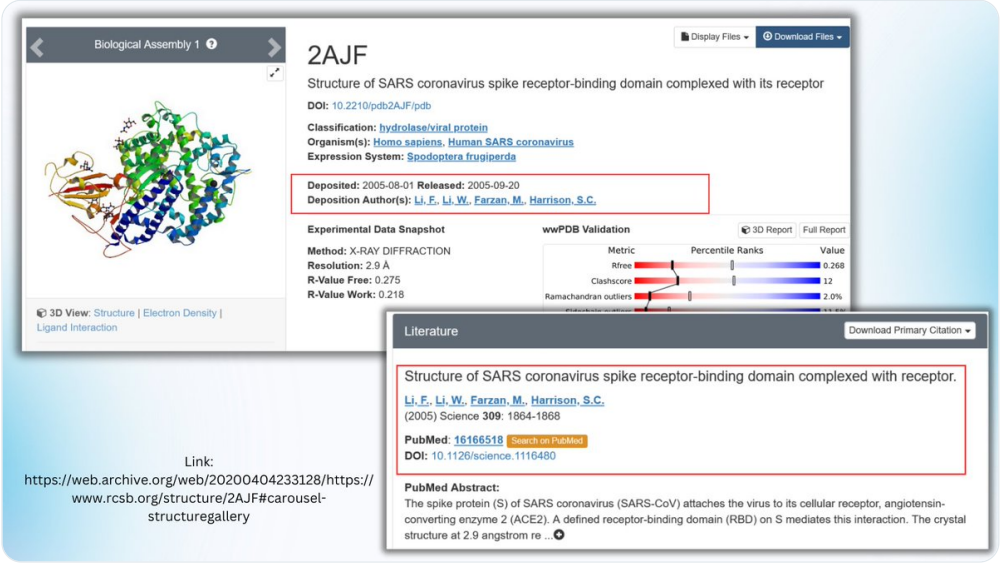
Biological Assembly 1
2AJF
Structure of SARS coronavirus spike receptor-binding domain complexed with its receptor
DOI: 10.2210/pdb2AJF/pdb
Classification: hydrolase/viral protein
Organism(s): Homo sapiens, Human SARS coronavirus
Expression System: Spodoptera frugiperda
Deposited: 2005-08-01 Released: 2005-09-20
Deposition Author(s): Li, F., Li, W., Farzan, M., Harrison, S.C.
Experimental Data Snapshot
Method: X-RAY DIFFRACTION
Resolution: 2.9 Å
R-Value Free: 0.275
R-Value Work: 0.218
wwPDB Validation
Metric
Percentile Ranks
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Clashscore
12
Ramachandran outliers
2.0%
3D View: Structure | Electron Density | Ligand Interaction
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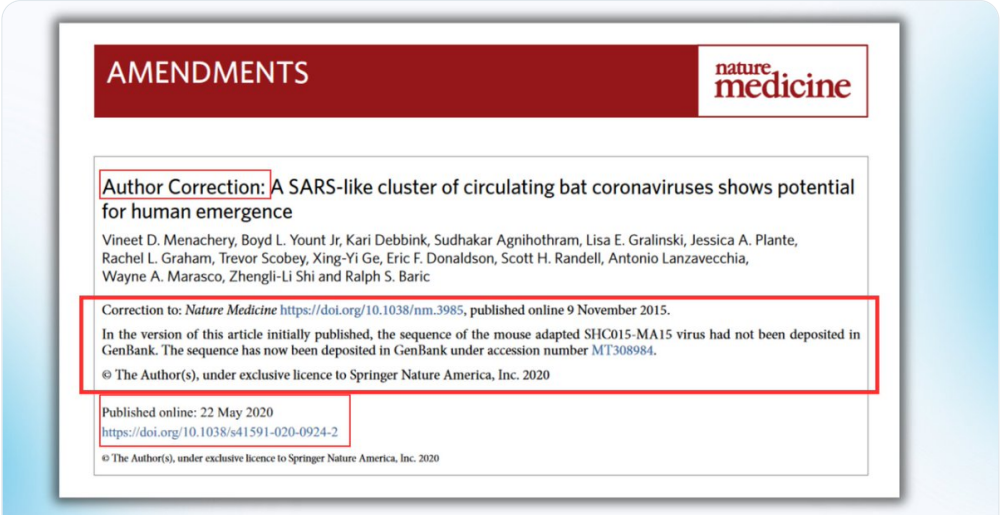
Li, F., Li, W., Farzan, M., Harrison, S.C.
(2005) Science 309: 1864-1868
PubMed: 16166518
DOI: 10.1126/science.1116480
PubMed Abstract:
The spike protein (S) of SARS coronavirus (SARS-CoV) attaches the virus to its cellular receptor, angiotensin-converting enzyme 2 (ACE2). A defined receptor-binding domain (RBD) on S mediates this interaction. The crystal structure at 2.9 angstrom re ...

Link: https://web.archive.org/web/20200404233128/https://www.rcsb.org/structure/2AJF#carousel-structuregallery

9 The 2020 Correction notice said "the version of this article initially published, the sequence of the mouse adapted SHC015-MA15 virus had not been deposited in GenBank. The sequence has now been deposited in GenBank under accession number MT308984." So, I checked MT308984



AMENDMENTS

nature medicine

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Vineet D. Menachery, Boyd L. Yount Jr, Kari Debbink, Sudhakar Agnihothram, Lisa E. Gralinski, Jessica A. Plante, Rachel L. Graham, Trevor Scobey, Xing-Yi Ge, Eric F. Donaldson, Scott H. Randell, Antonio Lanzavecchia, Wayne A. Marasco, Zhengli-Li Shi and Ralph S. Baric

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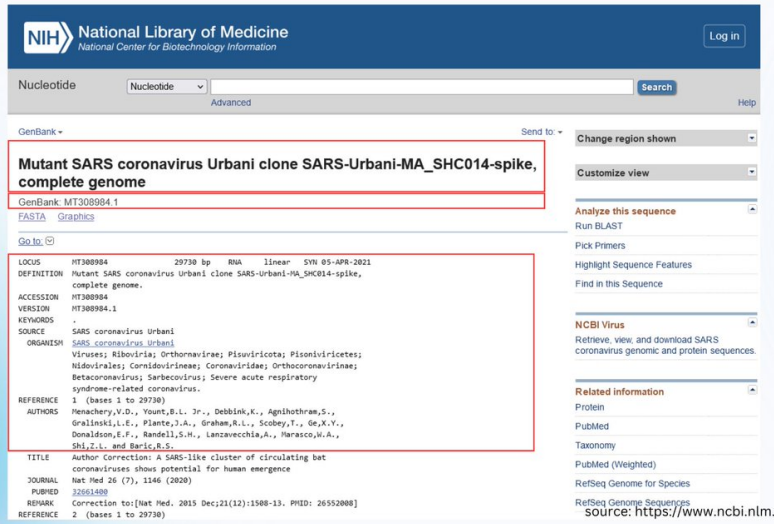
LINK: https://ratical.org/PandemicParallaxView/SARS-like-cluster-coronarius-2015.pdf



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Mutant SARS coronavirus Urbani clone SARS-Urbani-MA_SHC014-spike, complete genome

GenBank: MT308984.1

FASTA Graphics

Go to:

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LOCUS       MT308984              29730 bp    RNA     linear   SYN 05-APR-2021
DEFINITION  Mutant SARS coronavirus Urbani clone SARS-Urbani-MA_SHC014-spike,
            complete genome.
ACCESSION   MT308984
VERSION     MT308984.1
KEYWORDS    .
SOURCE      SARS coronavirus Urbani
  ORGANISM  SARS coronavirus Urbani
            Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;
            Nidovirales; Cornidovirineae; Coronaviridae; Orthocoronavirinae;
            Betacoronavirus; Sarbecovirus; Severe acute respiratory
            syndrome-related coronavirus.
REFERENCE   1  (bases 1 to 29730)
  AUTHORS   Menachery,V.D., Yount,B.L. Jr., Debbink,K., Agnihothram,S.,
            Gralinski,L.E., Plante,J.A., Graham,R.L., Scobey,T., Ge,X.Y.,
            Donaldson,E.F., Randell,S.H., Lanzavecchia,A., Marasco,W.A.,
            Shi,Z.L. and Baric,R.S.
  TITLE     Author Correction: A SARS-like cluster of circulating bat
            coronaviruses shows potential for human emergence
  JOURNAL   Nat Med 26 (7), 1146 (2020)
   PUBMED   32661400
   REMARK   Correction to:[Nat Med. 2015 Dec;21(12):1508-13. PMID: 26552008]
REFERENCE   2  (bases 1 to 29730)
```

Change region shown | Customize view

Analyze this sequence
Run BLAST
Pick Primers
Highlight Sequence Features
Find in this Sequence

NCBI Virus
Retrieve, view, and download SARS coronavirus genomic and protein sequences.

Related information
Protein
PubMed
Taxonomy
PubMed (Weighted)
RefSeq Genome for Species
RefSeq Genome Sequences

source: https://www.ncbi.nlm.nih.gov/nuccore/MT308984

10 🧵 The sequence appears as it should complete with the citation of the correction and the author's names, Baric included. However, what it fails to do is highlight the MASSIVE failure in preforming even the most basic protocols of science, let alone in GoF!

11 🧵 Also, its interesting the Congress requested and did interview Dr.Farzan, to which I've yet to see the transcription but Farzan was mentioned in Bob Garry's testimony in June confirming the testimony occurred.

COMMITTEE ON OVERSIGHT AND ACCOUNTABILITY,

SELECT SUBCOMMITTEE ON THE CORONAVIRUS PANDEMIC,

U.S. HOUSE OF REPRESENTATIVES,

WASHINGTON, D.C.

INTERVIEW OF: ROBERT F. GARRY

Friday, June 9, 2023

New Orleans, Louisiana

The interview in the above matter was held at Tulane University Medical School, Hutchinson Building, 1430 Tulane Avenue, New Orleans, Louisiana, commencing at 8:57 a.m. Central Time.

LINK: https://oversight.house.gov/wp-content/uploads/2023/07/2023.06.09-Garry-Transcript-.pdf

page 163

A Was I aware by February 10th? I mean, I think not directly. But I think that I had indications indirectly that that possibly was going on.

Q What were those indications?

A I mean, just for example, the call that I got from somebody at the White House. I can't remember exactly who it was or what they were doing, but it seemed to imply that there were other folks looking into this.

Q We can move on from those and move to Dr. Farzan. We'll go back to majority exhibit 13, which is the actual published version of "Proximal Origin."

A Okay.

Q On the last page, in the "Acknowledgments" section, it says, "We thank M.

164

Farzan for discussions." Is it your recollection that that's Michael Farzan?

A That's who it is, yes.

Q Okay. When asked during a transcribed interview if Dr. Farzan was aware that Dr. Andersen, you, Dr. Rambaut, and Dr. Holmes were going to acknowledge him at the end of the paper, he responded, "I was not aware of that prior to publication."

Did you know prior to publication that Dr. Farzan was going to be acknowledged on the paper?

A I signed off on the paper. I mean, he's not a direct colleague of mine. He's a colleague of Kristian Andersen. They're at the same institution, so --

Mr. Pellegrini. I'm sorry, Dr. Garry. Can you speak up a little bit?

Dr. Garry. I'm sorry. He's not at my institution. He's at Scripps Research, which is where Kristian Andersen is. So I didn't think too much of it when the acknowledgment was put in.

BY MR. BENZINE:

https://oversight.house.gov/wp-content/uploads/2023/07/2023.06.09-Garry-Transcript-.pdf

page 164

Q For the record -- and you would have probably no way of knowing this -- Dr. Farzan doesn't work at Scripps Research anymore. He works at Boston Children's Hospital.

A Oh, okay. Great. He did work there.

Q Yes, he did.

A Okay.

Q He did during this time. He worked at Scripps.

A Okay. All right. Great.

Q Did you have any discussions with Michael Farzan while drafting "Proximal Origin"?

A I did not.

165

Q Is it common practice to acknowledge people without their knowledge or permission?

A It's not common practice.

Q Okay. Do you have any knowledge of why Dr. Andersen would've done it in this case?

A I have no knowledge.

Q Is Dr. Farzan influential in coronaviruses and specifically SARS-related coronaviruses?

A He is. He discovered the receptor was ACE2 for the first SARS. Yeah.

Q Is it possible that Dr. Andersen, much like with Dr. Lipkin, wanted to add gravitas to the paper by acknowledging Dr. Farzan?

A I mean, you'd have to ask Dr. Andersen about that, but, you know, in the sense that anything's possible, it's possible, yeah.

https://oversight.house.gov/wp-content/uploads/2023/07/2023.06.09-Garry-Transcript-.pdf

12 🧵 Garry testifies that Farzan was among the few scientists the Proximal Origins authors wanted to discuss the sticky situation in early 2020. Garry opines that Farzan was called upon due to Andersen, since they both work at Scripps. Oddly so did Ian Lipkin.

page 164

Q For the record -- and you would have probably no way of knowing this -- Dr. Farzan doesn't work at Scripps Research anymore. He works at Boston Children's Hospital.

A Oh, okay. Great. He did work there.

Q Yes, he did.

A Okay.

Q He did during this time. He worked at Scripps.

A Okay. All right. Great.

Q Did you have any discussions with Michael Farzan while drafting "Proximal Origin"?

A I did not.

165

Q Is it common practice to acknowledge people without their knowledge or permission?

A It's not common practice.

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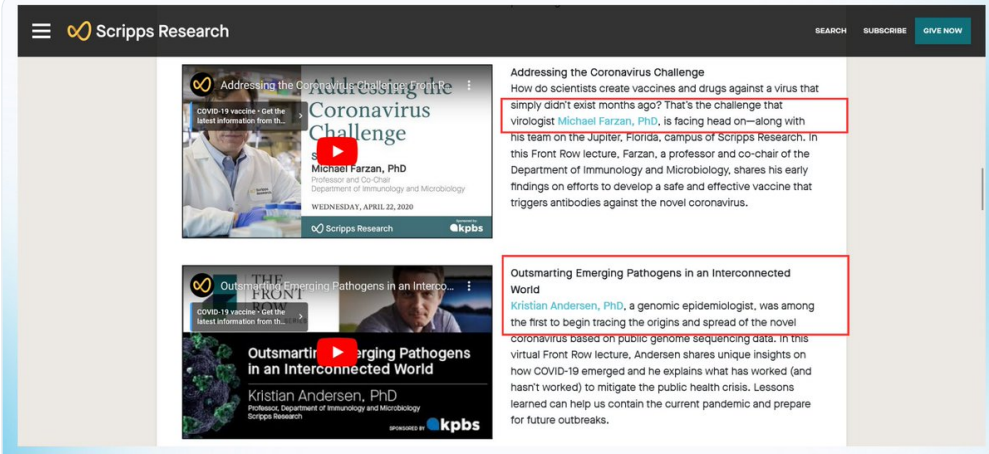
A He is. He discovered the receptor was ACE2 for the first SARS. Yeah.

Q Is it possible that Dr. Andersen, much like with Dr. Lipkin, wanted to add gravitas to the paper by acknowledging Dr. Farzan?

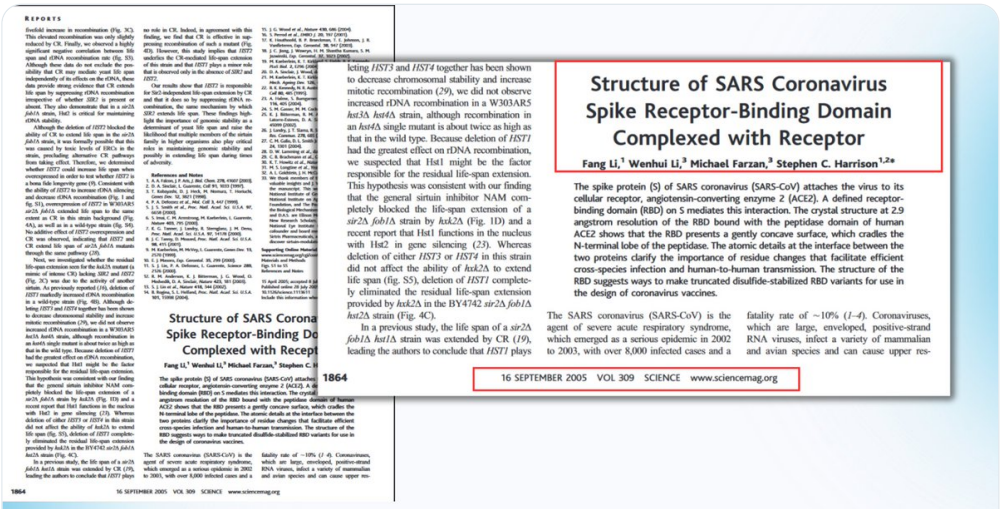
A I mean, you'd have to ask Dr. Andersen about that, but, you know, in the sense that anything's possible, it's possible, yeah.

https://oversight.house.gov/wp-content/uploads/2023/07/2023.06.09-Garry-Transcript-.pdf

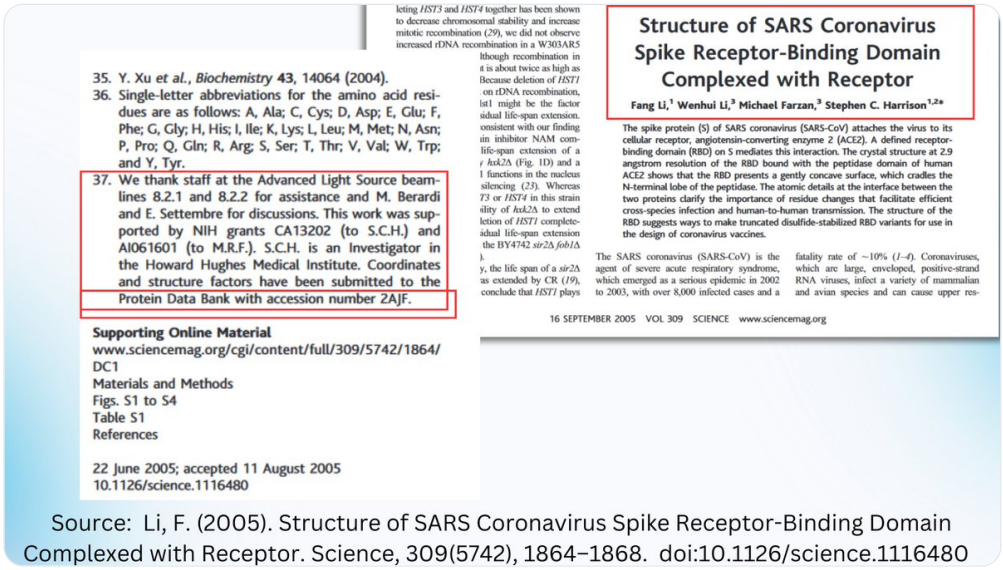
13🧵 Farzan according to Garry was the one to "discover the receptor ACE2 [sic..] was for the first SARS." The question is, HOW would we know if C19 came from Baric's Frankenstein experiments if the genome wasn't uploaded until AFTER the pandemic was active?


Scripps Research
SEARCH
SUBSCRIBE
GIVE NOW
Addressing the Coronavirus Challenge
Michael Farzan, PhD
Professor and Co-Chair
Department of Immunology and Microbiology
WEDNESDAY, APRIL 22, 2020
Scripps Research
kpbs
Addressing the Coronavirus Challenge
How do scientists create vaccines and drugs against a virus that simply didn't exist months ago? That's the challenge that virologist Michael Farzan, PhD, is facing head on—along with his team on the Jupiter, Florida, campus of Scripps Research. In this Front Row lecture, Farzan, a professor and co-chair of the Department of Immunology and Microbiology, shares his early findings on efforts to develop a safe and effective vaccine that triggers antibodies against the novel coronavirus.
Outsmarting Emerging Pathogens in an Interconnected World
Kristian Andersen, PhD
Professor, Department of Immunology and Microbiology
Scripps Research
kpbs
Outsmarting Emerging Pathogens in an Interconnected World
Kristian Andersen, PhD, a genomic epidemiologist, was among the first to begin tracing the origins and spread of the novel coronavirus based on public genome sequencing data. In this virtual Front Row lecture, Andersen shares unique insights on how COVID-19 emerged and he explains what has worked (and hasn't worked) to mitigate the public health crisis. Lessons learned can help us contain the current pandemic and prepare for future outbreaks.

Source: https://www.scripps.edu/covid-19/videos/


REPORTS
Structure of SARS Coronavirus Spike Receptor-Binding Domain Complexed with Receptor
Fang Li,[1] Wenhui Li,[3] Michael Farzan,[3] Stephen C. Harrison[1,2]*
The spike protein (S) of SARS coronavirus (SARS-CoV) attaches the virus to its cellular receptor, angiotensin-converting enzyme 2 (ACE2). A defined receptor-binding domain (RBD) on S mediates this interaction. The crystal structure at 2.9 angstrom resolution of the RBD bound with the peptidase domain of human ACE2 shows that the RBD presents a gently concave surface, which cradles the N-terminal lobe of the peptidase. The atomic details at the interface between the two proteins clarify the importance of residue changes that facilitate efficient cross-species infection and human-to-human transmission. The structure of the RBD suggests ways to make truncated disulfide-stabilized RBD variants for use in the design of coronavirus vaccines.
1864
16 SEPTEMBER 2005 VOL 309 SCIENCE www.sciencemag.org

Source: Li, F. (2005). Structure of SARS Coronavirus Spike Receptor-Binding Domain Complexed with Receptor. Science, 309(5742), 1864–1868. doi:10.1126/science.1116480



leting *HST3* and *HST4* together has been shown to decrease chromosomal stability and increase mitotic recombination (*29*), we did not observe increased rDNA recombination in a W303AR5

lthough recombination in
t is about twice as high as
Because deletion of *HST1*
on rDNA recombination,
lst1 might be the factor
sidual life-span extension.
consistent with our finding
in inhibitor NAM com-
life-span extension of a
*hxk2*Δ (Fig. 1D) and a
l functions in the nucleus
silencing (*23*). Whereas
73 or *HST4* in this strain
ility of *hxk2*Δ to extend
letion of *HST1* complete-
sidual life-span extension
the BY4742 *sir2*Δ *fob1*Δ
).
y, the life span of a *sir2*Δ
as extended by CR (*19*),
conclude that *HST1* plays

35. Y. Xu *et al.*, *Biochemistry* **43**, 14064 (2004).
36. Single-letter abbreviations for the amino acid residues are as follows: A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.
37. We thank staff at the Advanced Light Source beamlines 8.2.1 and 8.2.2 for assistance and M. Berardi and E. Settembre for discussions. This work was supported by NIH grants CA13202 (to S.C.H.) and AI061601 (to M.R.F.). S.C.H. is an Investigator in the Howard Hughes Medical Institute. Coordinates and structure factors have been submitted to the Protein Data Bank with accession number 2AJF.

Supporting Online Material
www.sciencemag.org/cgi/content/full/309/5742/1864/DC1
Materials and Methods
Figs. S1 to S4
Table S1
References

22 June 2005; accepted 11 August 2005
10.1126/science.1116480

Structure of SARS Coronavirus Spike Receptor-Binding Domain Complexed with Receptor

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The SARS coronavirus (SARS-CoV) is the agent of severe acute respiratory syndrome, which emerged as a serious epidemic in 2002 to 2003, with over 8,000 infected cases and a

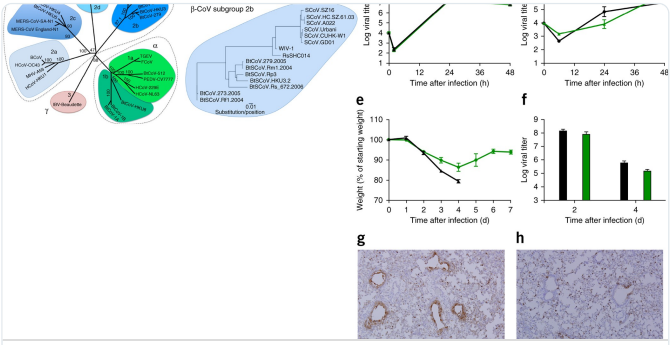
fatality rate of ~10% (*1*–*6*). Coronaviruses, which are large, enveloped, positive-strand RNA viruses, infect a variety of mammalian and avian species and can cause upper res-

Source: Li, F. (2005). Structure of SARS Coronavirus Spike Receptor-Binding Domain Complexed with Receptor. Science, 309(5742), 1864–1868. doi:10.1126/science.1116480

14 Baric, inventor the "No-See Um" sites- already tried to hied ties to Wuhan & Eco Health. -they hid the chimera's genome from public eyes.-they didn't correct this until 4 & 1/2 months AFTER C19 was sequenced, which was uploaded by on one the proximal origin authors[Holmes] ..

15 ...and even that paper was a sham! It makes me wonder about what really happened to Dr. Rashid Buttar, who was the first to warn people about this research in April of 2020.

https://ratical.org/PandemicParallaxView/SARS-like-cluster-coronarius-2015.pdf



A SARS-like cluster of circulating bat coronaviruses shows potential ...
Ralph Baric, Vineet Menachery and colleagues characterize a SARS-like coronavirus circulating in Chinese horseshoe bats to determine its potential to infect primary human airway epithelial cells, cau…

https://www.nature.com/articles/nm.3985

en.wikipedia.org/wiki/SHC014-CoV
https://www.nature.com/articles/nm0416-446a.pdf
https://oversight.house.gov/wp-content/uploads/2023/07/2023.06.09-Garry-Transcript-.pdf
https://web.archive.org/web/20200404233128/https://www.rcsb.org/structure/2AJF#carousel-structuregallery
https://www.scripps.edu/covid-19/videos/
https://www.ncbi.nlm.nih.gov/nuccore/MT308984

A SARS-like cluster of circulating bat coronaviruses shows potential f
Ralph Baric, Vineet Menachery and colleagues characterize a SARS-like coronavirus circulating in Chinese horseshoe bats to determine its potential to infect primary human airway epithelial cells, cau…

https://web.archive.org/web/20200315024135/https://www.nature.com/articles/nm.39…

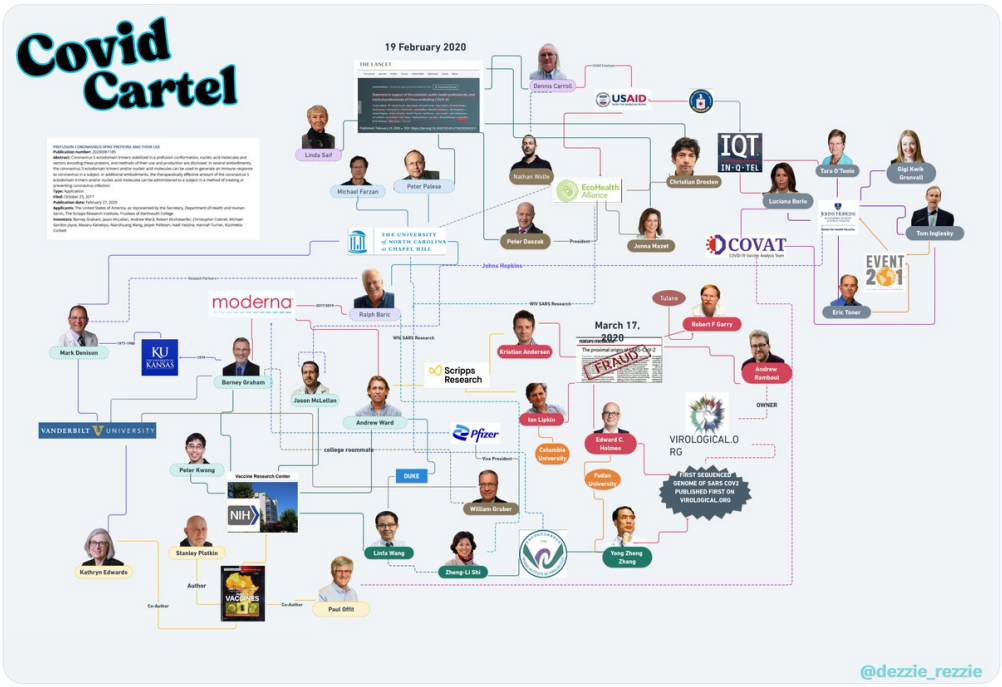
@P_McCulloughMD @DrJudyAMikovits @carolina_bonita @naomirwolf @Jikkyleaks @stkirsch @StealthMedical1 @RandPaul @AaronKheriatyMD @AaronSiriSG @ChildrensHD @whitematador @azen03 @Nuni_Sas_Yu @TLAVagabond @drcole12 @RyanMattaMedia @zeke_vegas @drdrew @welcometheeagle @Truthseeker070

• • •

Destiny Rezendes @dezzie_rezzie

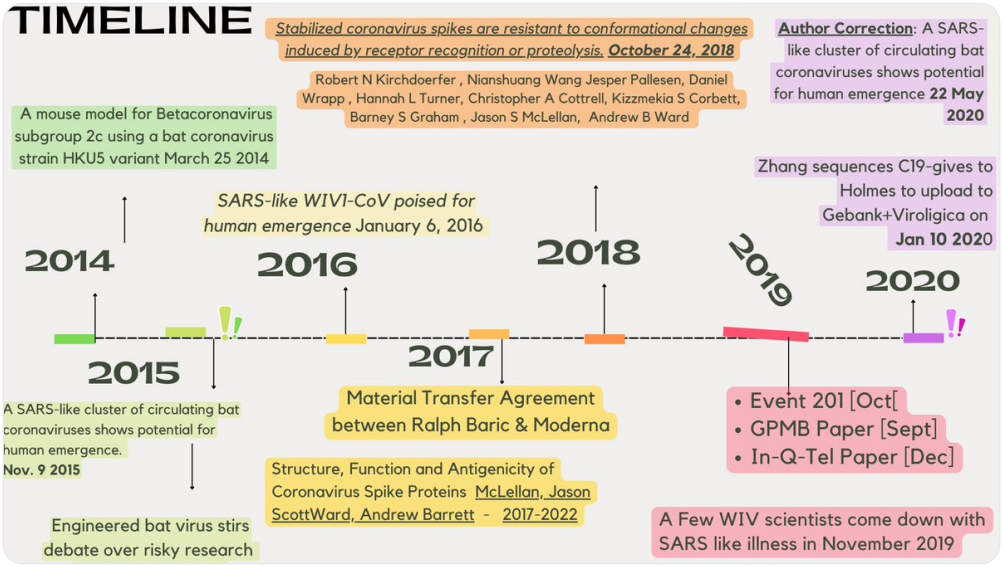
Nov 30, 2023 · 13 tweets · dezzie_rezzie/status/1730357442389651712

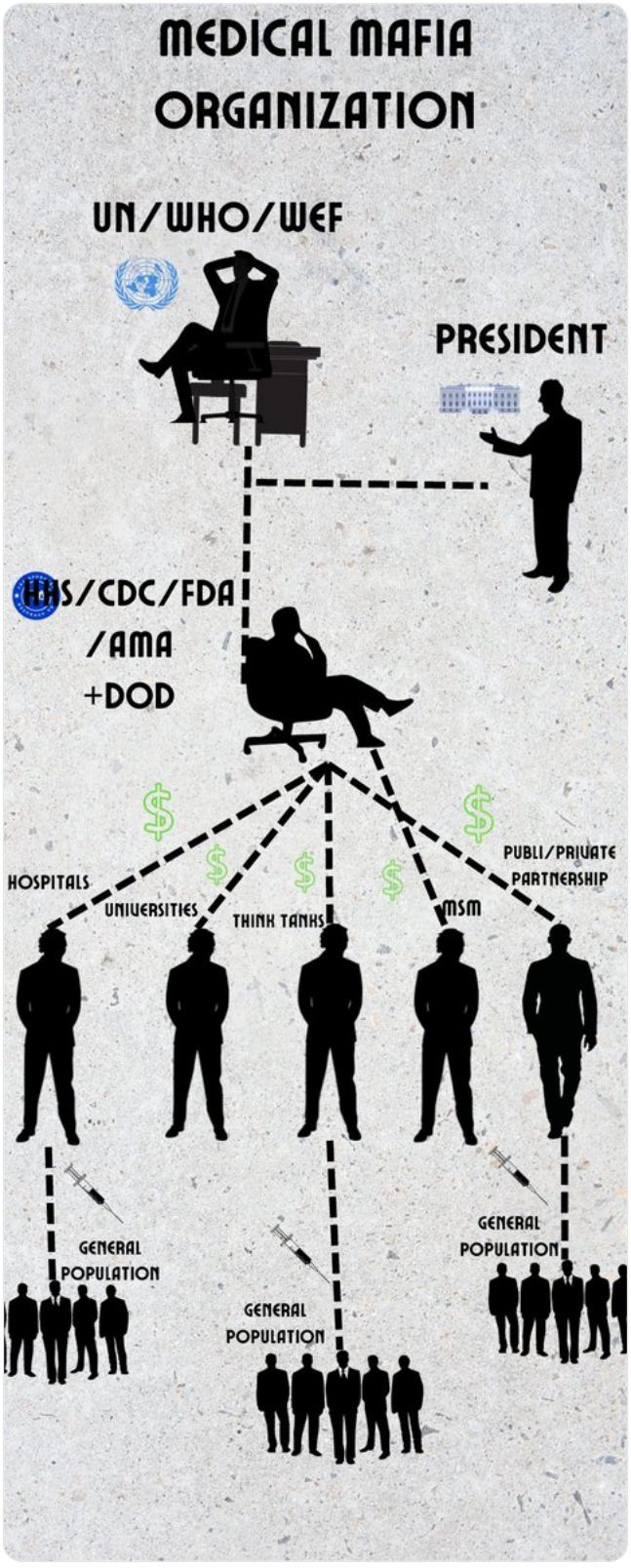
🧵1🏆 TBH I have struggled w/ how to present all this C19 information for a while. By the end of this thread hopefully I make something apparent: those who benefited by the pandemic wasn't by chance.



2🧵The timeline I'm focusing on largely pre-dates C19 [2014-2019] After seeing the connections fully flushed out it no longer becomes a question of 'if' or 'why'. All that remains is what is to be done about it.

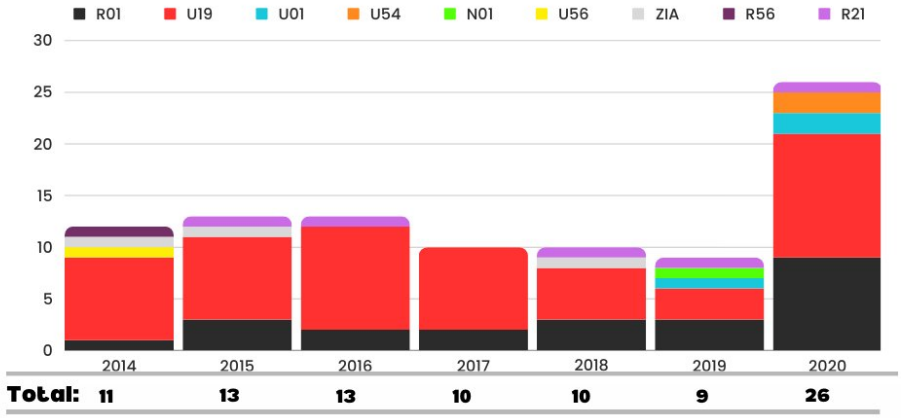
Photograph: EcoHealth Alliance president Peter Daszak, above right, with the Wuhan Institute of Virology's Shi Zhengli, centre, and CSIRO's Linfa Wang, second from right, circa 2005 and taken from a now deleted page on the Wuhan institute's website.


TIMELINE
Stabilized coronavirus spikes are resistant to conformational changes induced by receptor recognition or proteolysis. October 24, 2018
Robert N Kirchdoerfer , Nianshuang Wang Jesper Pallesen, Daniel Wrapp , Hannah L Turner, Christopher A Cottrell, Kizzmekia S Corbett, Barney S Graham , Jason S McLellan, Andrew B Ward
Author Correction: A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence 22 May 2020
A mouse model for Betacoronavirus subgroup 2c using a bat coronavirus strain HKU5 variant March 25 2014
Zhang sequences C19-gives to Holmes to upload to Gebank+Viroligica on Jan 10 2020
SARS-like WIV1-CoV poised for human emergence January 6, 2016
2014
2015
2016
2017
2018
2019
2020
A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. Nov. 9 2015
Engineered bat virus stirs debate over risky research
Material Transfer Agreement between Ralph Baric & Moderna
Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason ScottWard, Andrew Barrett - 2017-2022
• Event 201 [Oct[
• GPMB Paper [Sept]
• In-Q-Tel Paper [Dec]
A Few WIV scientists come down with SARS like illness in November 2019



3🧵I looked into Ralph Baric's grant history from 2014-2020. As you can see there was a noticeable increase in NIH grants to Baric when 2020 came around. His top collaborators were Denison [Vanderbilt] & Lipkin [Columbia] in those 7yrs.

RALPH BARIC NIH GRANTS 2014-2020



Total:	11	13	13	10	10	9	26

Total Grants [over 7 years]= 92 Grants

- Average Grants per Year= 13 per year
- 2020 received double the grants [26]over the 7 year avg [13]

83.69% of all grants are either R01 & U19 {77/92}

58% of all grants are just U19 {54/92}

Grant Type [7yrs]: 92 Total Grants made of 9 different types.

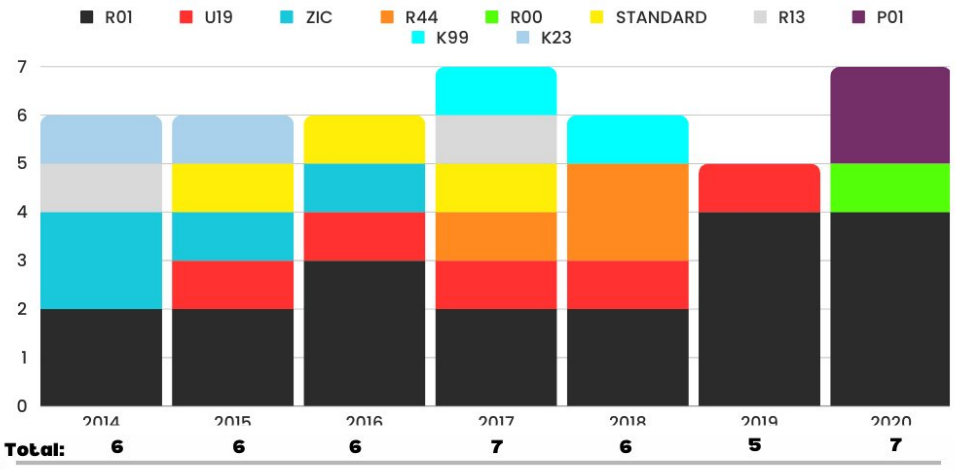
U19 [54], R01 [23], R21 [5], U01 [3], ZIA [3], U54 [2], N01 [1], R56 [1]

Institutions & Scientists from Ralph Baric's NIH Grants [2014-2020]

University of Texas Austin [2]	George Georgiou
University of Maryland College Park [2]	Anne Elizabeth Simon
University of California Berkeley [1]	Eva Harris
Vanderbilt University [8]	Mark Denison
Columbia University NY[8]	Ian Lipkin
Columbia University [2]	Ian Lipkin
Stanford [1]	Calvin Kuo, Manuel Amieva
Washington University [1]	Michael Diamond, James Crowe
NIAID Extramural [3]	Peter Jahrling
University of NC Chapel HIll [65]	Mark Heise, Timothy Sheahan Fang-Li

4🧵Andrew Ward [Scripps, Johns Hopkins, Vaccine Research Center] is a quietly mentioned but integral scientist credited w/ creation of the C19 jabs. Top grants yrs were 2017&2020, top collab's were Scripps, Vanderbilt, UT Austin.

ANDREW WARD NIH GRANTS 2014-2020



Total:	6	6	6	7	6	5	7

Total Grants [over 7 years]= 43 Grants

- **Average Grants per Year= 6 per year**
- **2020 & 2017 were the only two[both 7] above the 7 year avg [6]**

Grant Type [7yrs]: 43 Total Grants made of 10 different types.

U19 [5], R01 [19], R13 [2], R00 [1], ZIC [4], K99 [2], P01 [2], STANDARD[3], R44 [3]K23[2]

38 Scientists co-authored from 16 Institutions w/Andrew Ward's NIH Grants [2014-2020]

University of Texas Austin [3]
University of Pittsburgh [3]
Scripps Research [13]
Vanderbilt University [5]
Columbus State Community College[1]
Dartmouth University [1]
U.S. National Inst of Environ Hlth Scis[1]
University of Wisconsin-Madison [1]
Cornell University [2]
Keystone Symposia [2]
Denovx, LLC [3]]
Humboldt State University[1]
Harvard [1]
U.S. National Heart [3]
University of Texas Health Sci Center[1]
Oregon Health and Science Univ [2]

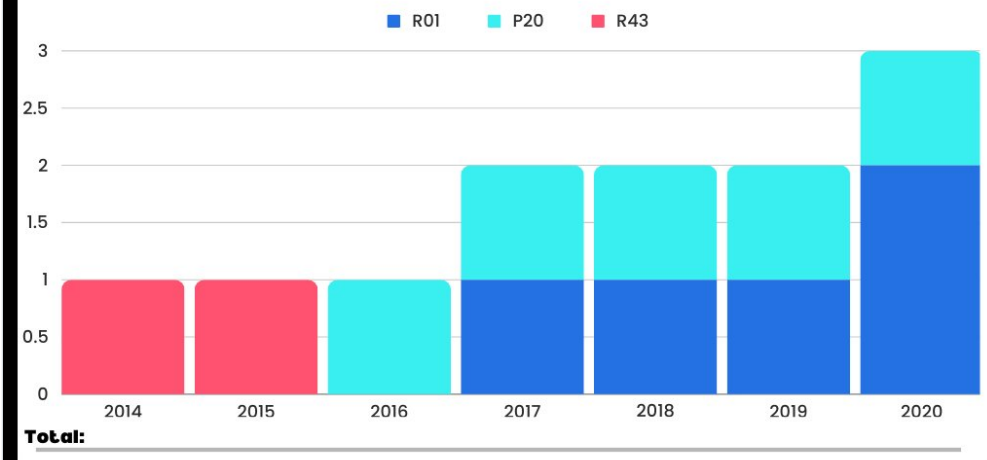
Ian Wilson ArdemPatapoutian
Shane Crotty,Jason McLellan
Andrew Hinck
Andrew Ward Lars Hangartne
Andrew Ward
Rogiers, Gloria; Clark, Gary; Ippolito, Joseph; Kerr, Andrew; Williams-Ward, Britney; Neuman, Arthu
Jason McLellan
James W Putney
Robert Kirchdoerfer
Ian Wilson John Moore
David Woodland Thale Cross Jarvis
Andrew Bond
Andrew Kinzinger, Craig Sean
Andrew Strominger
Michael Sack Andrew Arari
Andrew Hinck
Joseph El Youssef,

Institutions from ANDREW WARD'S NIH Grants [2014-2020]

13	Scripps Research Institute
5	Vanderbilt University Medical Center
3	University of Texas Austin
3	Denovx, LLC
3	University of Pittsburgh
3	U.S. National Heart Lung and Blood Inst
2	Weill Medical College of Cornell University
2	Oregon Health and Science University
2	Keystone Symposia
1	University of Wisconsin Madison
1	Dartmouth College
1	University of Texas Health Science Center
1	U.S. National Inst of Environ Hlth Scis
1	Columbus State Community College
1	Harvard University
1	Humboldt State Un

5🧵Jason McLellan, like Ward is a rarely mentioned yet integral architect of the C19 Vaccines, both w/patents crediting them. McLellan's NIH grants doubled after 2017. Top collab's are UT Austin & Dartmouth University.

JASON MCLELLAN NIH GRANTS 2014-2020



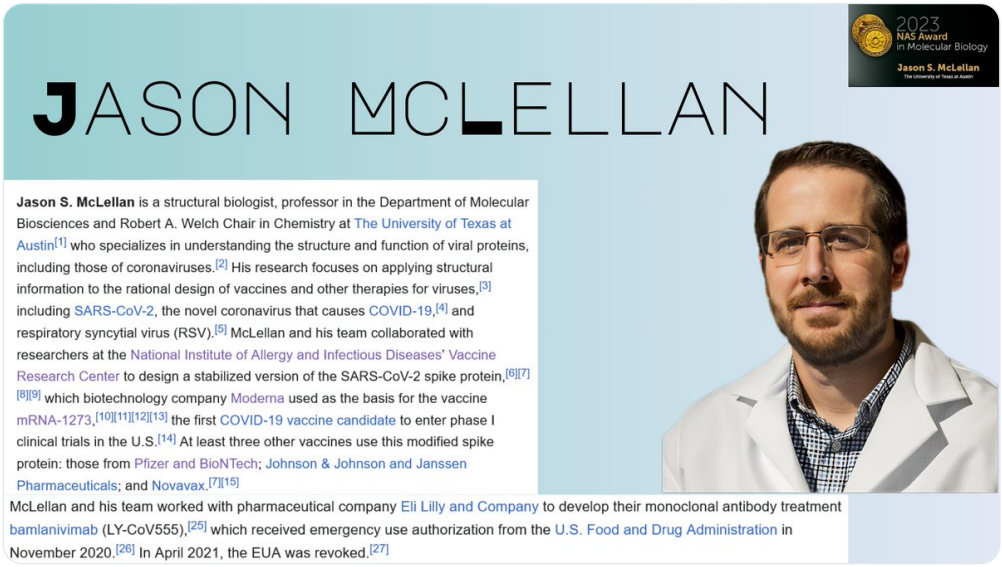
Total Grants 12 [over 7 years]= 4 per year avg

Grant Type [7yrs]: 12 Total Grants made of 3 different types.

P20 [5], R01 [5], R43 [2]

Scientists Institutions w/ Jason McLellan's NIH Grants [2014-2020]

University of Texas Austin [4]	**Kartik Chandran** **Andrew Ward**
Dartmouth University [6]	**Andrew Ward**
Avatar Medical [2]	**Roberto Mariano** **Mark Yondola**


2023
NAS Award
in Molecular Biology
Jason S. McLellan
JASON MCLELLAN
Jason S. McLellan is a structural biologist, professor in the Department of Molecular Biosciences and Robert A. Welch Chair in Chemistry at The University of Texas at Austin[1] who specializes in understanding the structure and function of viral proteins, including those of coronaviruses.[2] His research focuses on applying structural information to the rational design of vaccines and other therapies for viruses,[3] including SARS-CoV-2, the novel coronavirus that causes COVID-19,[4] and respiratory syncytial virus (RSV).[5] McLellan and his team collaborated with researchers at the National Institute of Allergy and Infectious Diseases' Vaccine Research Center to design a stabilized version of the SARS-CoV-2 spike protein,[6][7][8][9] which biotechnology company Moderna used as the basis for the vaccine mRNA-1273,[10][11][12][13] the first COVID-19 vaccine candidate to enter phase I clinical trials in the U.S.[14] At least three other vaccines use this modified spike protein: those from Pfizer and BioNTech; Johnson & Johnson and Janssen Pharmaceuticals; and Novavax.[7][15]
McLellan and his team worked with pharmaceutical company Eli Lilly and Company to develop their monoclonal antibody treatment bamlanivimab (LY-CoV555),[25] which received emergency use authorization from the U.S. Food and Drug Administration in November 2020.[26] In April 2021, the EUA was revoked.[27]

6🧵All these people converge with the Vaccine Research Center, an NIH component-most notable w/the head scientist, Barney Graham. In 2021, Graham & team explain to new POTUS Biden how the Vaxx came to be. Listen & Watch Closely. [*listen for 2017, & Moderna]

7🧵I transcribed the key parts in the attached images: Graham tell Biden that the Vaccine Research Center [VRC] made a deal & formal partnership in 2017 to work on a coronavirus prototype. Also in 2017 was the Material Transfer Agreement [MTA] between VRC & Moderna on CoV tech.

C-SPAN

February 11th 2021

Biden visits the NIH's Vaccine Research Center [VRC] to talk to scientists who helped created the C19 Vaccines. Barney Graham & Kizzmekia Corbett. Graham shows off a structural model of the C19 spike protein .

FEBRUARY 11, 2021

National Institutes of Health Viral Pathogenesis Laboratory

President Biden visited the Viral Pathogenesis Laboratory at the National Institutes of Health (NIH) in Bethesda, Maryland. He spoke with Viral Pathogenesis Lab Chief Dr. Barney Graham and COVID-19 Vaccine Program Scientific Lead Kizzmekia Corbett. They discussed development of the vaccine and challenges posed by the coronavirus variants. NIH Director Dr. Francis Collins and National Institute of Allergy and Infectious Diseases Director Dr. Anthony Fauci joined the president on the tour. close

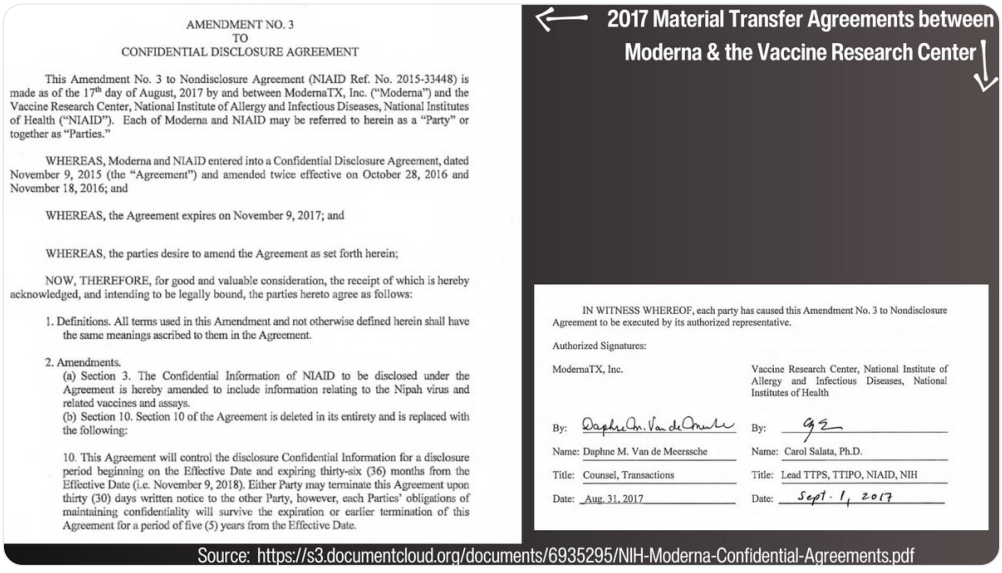
Source: https://www.c-span.org/video/?508940-1/national-institutes-health-viral-pathogenesis-laboratory

Graham speaking to President Biden:

"*Okay, so we helped them with some of their animal studies. We were making one kind of vaccine. They were making an MRNA vaccine. We learned that their technology was good. And so we made a deal in 2017 to work on Paramyxovirus is with the prototype and with coronavirus is with the prototype, Which is that MERS coronavirus? I'm okay. We've been working with Moderna's In a formal collaboration since 2017.*"

President Biden speakin the VRC staff & referring to Dr. Jeffery Zients:

"I realized that one of the things is that, you know, it's amazing how quickly things change in terms of people's perceptions. Mine, mine included. I know it's a little tiny bit about this because I worked with that guy on cancer issues for a long while can start with cancer. And he said to anyway, but what I didn't realize was just how much for the vaccine we're going to have to actually get produced. That's one thing that the vaccine, it's another thing to vaccinate tours, uh, put in people's arms and it's really turned out to be a gigantic logistical issue for. And I can say don't mean as a christian, there's an observation when we We've been office now three years, 3 weeks. "



AMENDMENT NO. 3
TO
CONFIDENTIAL DISCLOSURE AGREEMENT

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10. This Agreement will control the disclosure Confidential Information for a disclosure period beginning on the Effective Date and expiring thirty-six (36) months from the Effective Date (i.e. November 9, 2018). Either Party may terminate this Agreement upon thirty (30) days written notice to the other Party, however, each Parties' obligations of maintaining confidentiality will survive the expiration or earlier termination of this Agreement for a period of five (5) years from the Effective Date.

2017 Material Transfer Agreements between Moderna & the Vaccine Research Center

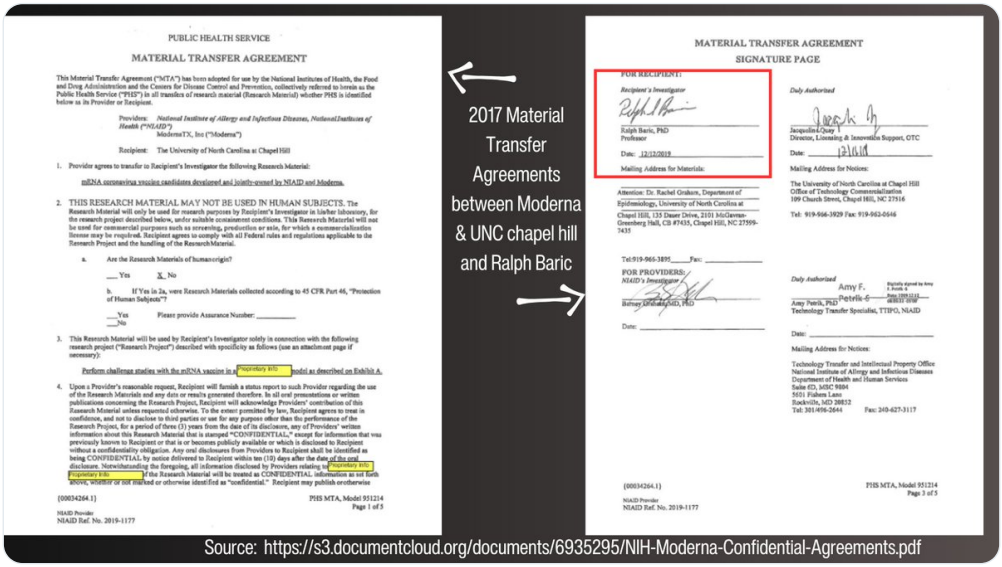
IN WITNESS WHEREOF, each party has caused this Amendment No. 3 to Nondisclosure Agreement to be executed by its authorized representative.

Authorized Signatures:

ModernaTX, Inc.	Vaccine Research Center, National Institute of Allergy and Infectious Diseases, National Institutes of Health
By: Daphne M. Van de Meerssche	By:
Name: Daphne M. Van de Meerssche	Name: Carol Salata, Ph.D.
Title: Counsel, Transactions	Title: Lead TTPS, TTIPO, NIAID, NIH
Date: Aug. 31, 2017	Date: Sept. 1, 2017

Source: https://s3.documentcloud.org/documents/6935295/NIH-Moderna-Confidential-Agreements.pdf

8🧵In that same MTA, later amended, Ralph Baric signs the MTA in 2019 for the same technology but read Amendment 3 carefully. According to the contract, the collaboration between VRC and Moderna didn't start in 2017, but rather on Nov 9, 2015.🔎🤫



PUBLIC HEALTH SERVICE

MATERIAL TRANSFER AGREEMENT

This Material Transfer Agreement ("MTA") has been adopted for use by the National Institutes of Health, the Food and Drug Administration and the Centers for Disease Control and Prevention, collectively referred to herein as the Public Health Service ("PHS") in all transfers of research material (Research Material) whether PHS is identified below as its Provider or Recipient.

Providers: *National Institute of Allergy and Infectious Diseases, National Institutes of Health ("NIAID")*
ModernaTX, Inc ("Moderna")

Recipient: The University of North Carolina at Chapel Hill

1. Provider agrees to transfer to Recipient's Investigator the following Research Material:

mRNA coronavirus vaccine candidates developed and jointly-owned by NIAID and Moderna.

2. THIS RESEARCH MATERIAL MAY NOT BE USED IN HUMAN SUBJECTS. The Research Material will only be used for research purposes by Recipient's Investigator in his/her laboratory, for the research project described below, under suitable containment conditions. This Research Material will not be used for commercial purposes such as screening, production or sale, for which a commercialization license may be required. Recipient agrees to comply with all Federal rules and regulations applicable to the Research Project and the handling of the Research Material.

a. Are the Research Materials of human origin?

___Yes X No

b. If Yes in 2a, were Research Materials collected according to 45 CFR Part 46, "Protection of Human Subjects"?

___Yes Please provide Assurance Number: _____
___No

3. This Research Material will be used by Recipient's Investigator solely in connection with the following research project ("Research Project") described with specificity as follows (use an attachment page if necessary):

Perform challenge studies with the mRNA vaccine in a Proprietary Info model as described on Exhibit A.

4. Upon a Provider's reasonable request, Recipient will furnish a status report to such Provider regarding the use of the Research Materials and any data or results generated therefore. In all oral presentations or written publications concerning the Research Project, Recipient will acknowledge Providers' contribution of this Research Material unless requested otherwise. To the extent permitted by law, Recipient agrees to treat in confidence, and not to disclose to third parties or use for any purpose other than the performance of the Research Project, for a period of three (3) years from the date of its disclosure, any of Providers' written information about this Research Material that is stamped "CONFIDENTIAL," except for information that was previously known to Recipient or that is or becomes publicly available or which is disclosed to Recipient without a confidentiality obligation. Any oral disclosures from Providers to Recipient shall be identified as being CONFIDENTIAL by notice delivered to Recipient within ten (10) days after the date of the oral disclosure. Notwithstanding the foregoing, all information disclosed by Providers relating to Proprietary Info Proprietary Info of the Research Material will be treated as CONFIDENTIAL information as set forth above, whether or not marked or otherwise identified as "confidential." Recipient may publish or otherwise

{00034264.1} PHS MTA, Model 951214
Page 1 of 5

NIAID Provider
NIAID Ref. No. 2019-1177

2017 Material Transfer Agreements between Moderna & UNC chapel hill and Ralph Baric

MATERIAL TRANSFER AGREEMENT
SIGNATURE PAGE

FOR RECIPIENT:

Recipient's Investigator

Ralph Baric, PhD
Professor

Date: 12/12/2019

Mailing Address for Materials:

Attention: Dr. Rachel Graham, Department of Epidemiology, University of North Carolina at Chapel Hill, 135 Dauer Drive, 2101 McGavran-Greenberg Hall, CB #7435, Chapel Hill, NC 27599-7435

Tel:919-966-3896 Fax: _____

FOR PROVIDERS:
NIAID's Investigator

Barney Graham, MD, PhD

Date: _____

Duly Authorized

Jacqueline Quay
Director, Licensing & Innovation Support, OTC

Date: 12/16/19

Mailing Address for Notices:

The University of North Carolina at Chapel Hill
Office of Technology Commercialization
109 Church Street, Chapel Hill, NC 27516

Tel: 919-966-3929 Fax: 919-962-0646

Duly Authorized

Amy Petrik, PhD

Digitally signed by Amy F. Petrik -S
Date: 2019.12.17 08:01:01 -05'00'

Technology Transfer Specialist, TTIPO, NIAID

Date: _____

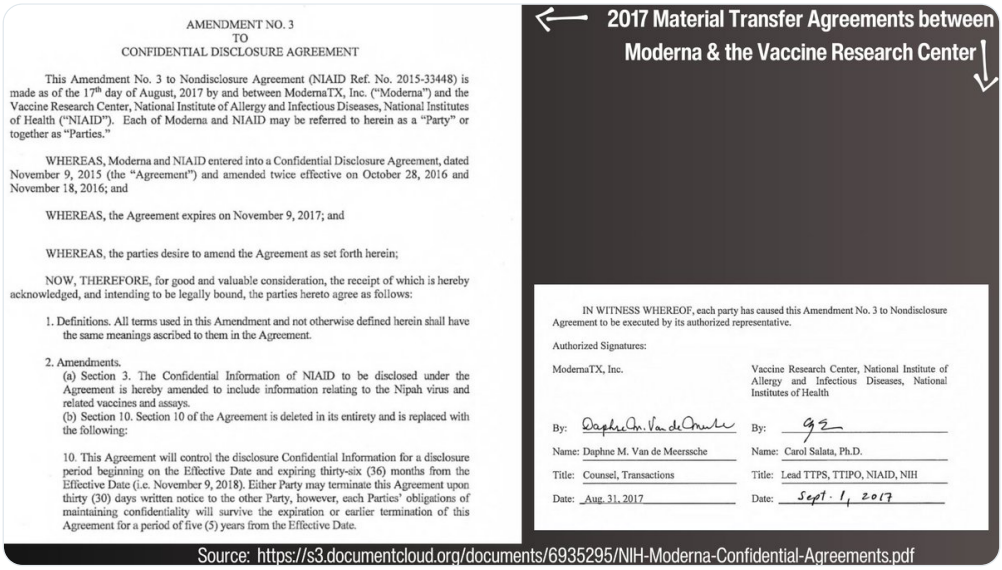
Mailing Address for Notices:

Technology Transfer and Intellectual Property Office
National Institute of Allergy and Infectious Diseases
Department of Health and Human Services
Suite 6D, MSC 9804
5601 Fishers Lane
Rockville, MD 20852
Tel: 3014956-2644 Fax: 240-627-3117

{00034264.1} PHS MTA, Model 951214
Page 3 of 5

NIAID Provider
NIAID Ref. No. 2019-1177

Source: https://s3.documentcloud.org/documents/6935295/NIH-Moderna-Confidential-Agreements.pdf



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By: Daphne M. Van de Meerssche	By:
Name: Daphne M. Van de Meerssche	Name: Carol Salata, Ph.D.
Title: Counsel, Transactions	Title: Lead TTPS, TTIPO, NIAID, NIH
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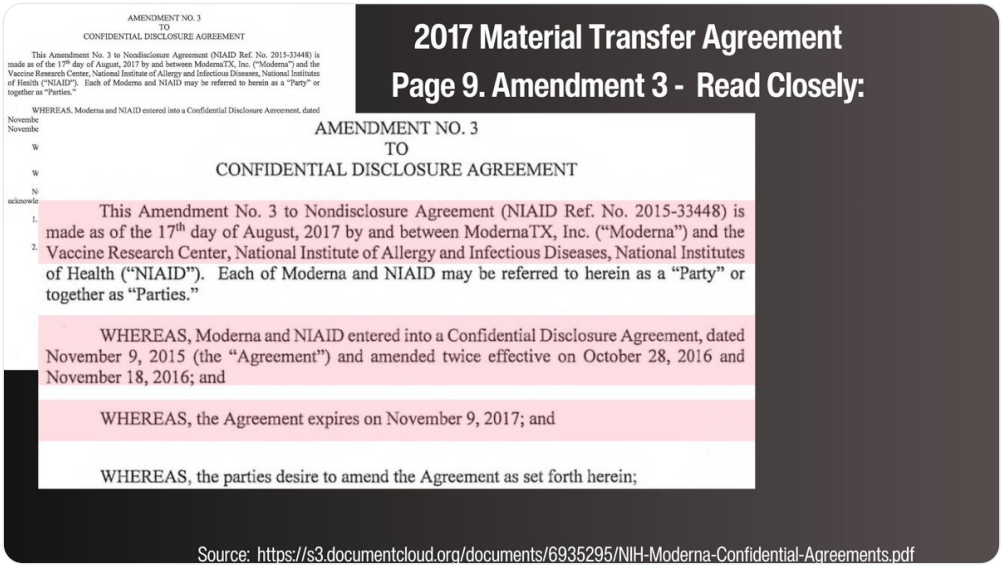
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9🧵That begs the question: Why claim the collab began in 2017, & what initiated the collab in November of 2015? You recall that paper in 2015 that got everyone worked up about GoF? The one by Ralph Baric & Shi-Zhengli where they created a chimeric SARS they neglected to upload ?

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

Abstract

The emergence of severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome (MERS)-CoV underscores the threat of cross-species transmission events leading to outbreaks in humans. Here we examine the disease potential of a SARS-like virus, SHC014-CoV, which is currently circulating in Chinese horseshoe bat populations[1]. Using the SARS-CoV reverse genetics system[2], we generated and characterized a chimeric virus expressing the spike of bat coronavirus SHC014 in a mouse-adapted SARS-CoV backbone. The results indicate that group 2b viruses encoding the SHC014 spike in a wild-type backbone can efficiently use multiple orthologs of the SARS receptor human angiotensin converting enzyme II (ACE2), replicate efficiently in primary human airway cells and achieve *in vitro* titers equivalent to epidemic strains of SARS-CoV. Additionally, *in vivo* experiments demonstrate replication of the chimeric virus in mouse lung with notable pathogenesis. Evaluation of available SARS-based immune-therapeutic and prophylactic modalities revealed poor efficacy; both monoclonal antibody and vaccine approaches failed to neutralize and protect from infection with CoVs using the novel spike protein. On the basis of these findings, we synthetically re-derived an infectious full-length SHC014 recombinant virus and demonstrate robust viral replication both *in vitro* and *in vivo*. Our work suggests a

10🧵 Oddly enough, something no one else has pointed out, that it happens to be that infamous article was published on Nature on November 9th 2015!💥🔎 THE SAME EXACT DAY as the MTA truly began with VRC & Moderna on a SARS-CoV vaccine prototype.

Vineet D Menachery, Boyd L Yount Jr, Kari Debbink, Sudhakar Agnihothram, Lisa E Gralinski,
A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence
Jessica A Plante, Rachel L Graham, Trevor Scobey, Xing-Yi Ge, Eric F Donaldson, Scott H Randell,
Antonio Lanzavecchia, Wayne A Marasco, Zhengli-Li Shi & Ralph S Baric

Nature Medicine **21**, 1508–1513 (2015) | Cite this article

2.84m Accesses | **559** Citations | **15792** Altmetric | Metrics

30 March 2020 Editors' note, March 2020: We are aware that this article is being used as the basis for unverified theories that the novel coronavirus causing COVID-19 was engineered. There is no evidence that this is true; scientists believe that an animal is the most likely source of the coronavirus.

An Author Correction to this article was published on 22 May 2020

A Corrigendum to this article was published on 06 April 2016

This article has been updated

Letter | Published: 09 November 2015

A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence

Vineet D Menachery, Boyd L Yount Jr, Kari Debbink, Sudhakar Agnihothram, Lisa E Gralinski, Jessica A Plante, Rachel L Graham, Trevor Scobey, Xing-Yi Ge, Eric F Donaldson, Scott H Randell, Antonio Lanzavecchia, Wayne A Marasco, Zhengli-Li Shi & Ralph S Baric

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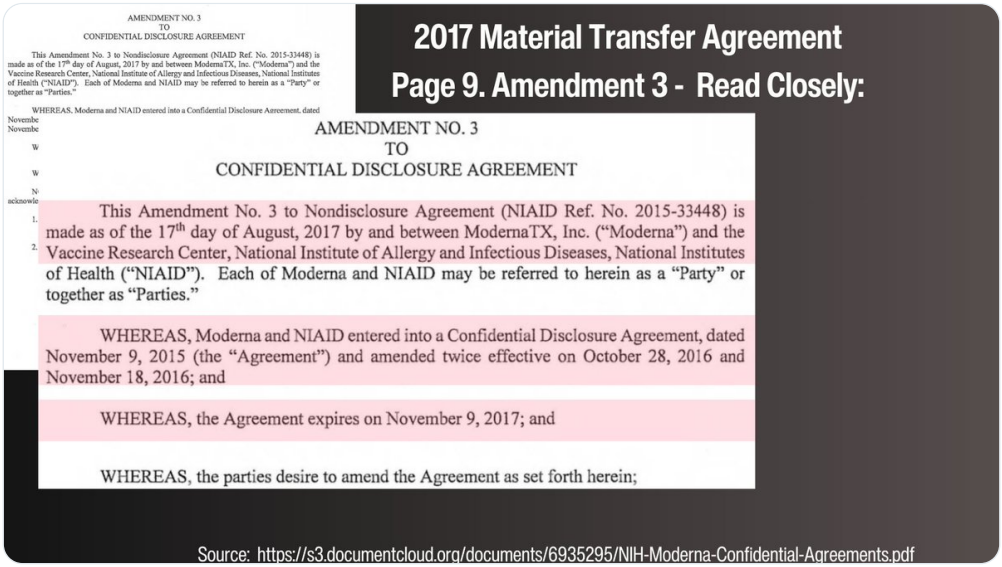
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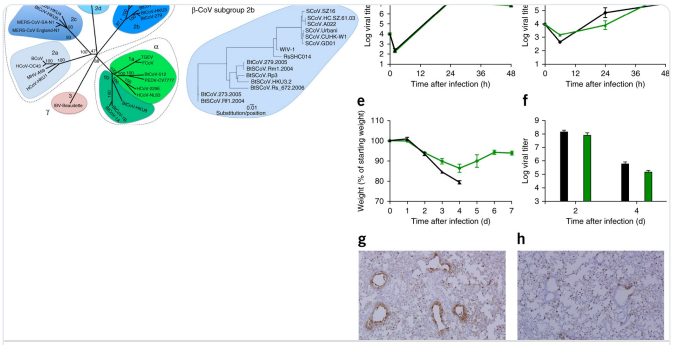
11🧵Maybe that's a coincidence, but look out for the part 2 because I'm not finished w/this. I do however want to make it digestible. Up next, the Patent rights, the Cancer money, & the enslaved University's Involved. Receipts:



A SARS-like cluster of circulating bat coronaviruses shows potential f…
Ralph Baric, Vineet Menachery and colleagues characterize a SARS-like coronavirus circulating in Chinese horseshoe bats to determine its potential to infect primary human airway epithelial cells, cau…
https://www.nature.com/articles/nm.3985#Ack1

https://s3.documentcloud.org/documents/6935295/NIH-Moderna-Confidential-Agreements.pdf

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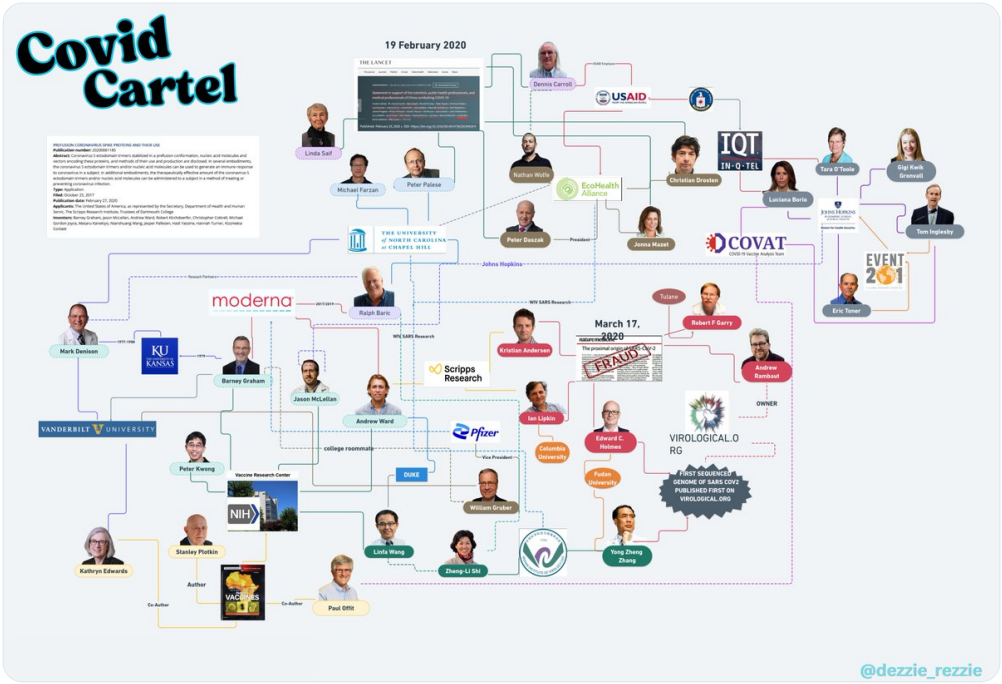
@DrDMartinWorld @DrJudyAMikovits @P_McCulloughMD @carolina_bonita @StealthMedical1 @jathorpmfm @Jikkyleaks @EcoHealthNYC @RandPaul @laralogan @TheRedactedInc @COVIDSelect @JeffereyJaxen @drcole12 @TLAVagabond @AaronKheriatyMD @AaronSiriSG 🙏

• • •

Destiny Rezendes @dezzie_rezzie

Dec 1, 2023 • 12 tweets • dezzie_rezzie/status/1730393042866115023

PART 2 🧵2017 Was a massively important year: VRC+ Moderna collab' on a CoV vaccine, USAID's Andrew Clements emailed EHA staff to move Metabiota from China & instead send EHA, the "PREFUSION CORONAVIRUS SPIKE PROTEINS" patent & a meeting at NIH w/Bill Gates & Graham...



2🧵June 30, 2017 NIH hosts the 4th annual meeting between Bill Gates & the VRC. Attendees included Gates, Graham, Fauci, Collins, and Mascola. The newsletter covering the event shows Graham holding what appears to be the spike protein to show Gates. -Identical to the 2021 one..

NIH RECORD

June 30, 2017
Vol. LXIX, No. 13

National Institutes of Health

ACD Supports Early Investigators, Applauds Collins' Reappointment

BY RICH MCMANUS

Two days before the 114th meeting of the advisory committee to the NIH director on June 8, the President invited NIH director Dr. Francis Collins to remain in that post permanently.

"I am grateful and honored to have received that invitation," said Collins, who had been serving as a holdover appointment since Jan. 18, "and I am happy, along with my wife Diane, to accept it."

The news was met with a round of applause before the ACD got down to a 2-day agenda that included announcement of the Next Generation of Researchers Initiative (NGRI) to support early and mid-career investigators; presentation of NIH's efforts to reduce the nation's opioid epidemic; and an argument for an accelerated pathway toward a universal influenza vaccine.

NIH director Dr. Francis Collins (l), flanked by ACD member Dr. Jose Florez of the Broad Institute of MIT and Harvard, told the group that he thought last December's ACD meeting might have been his last.

Not Ready for Prime Time

Collins traced the half-year history of the effort to reallocate NIH funding for early and mid-career scientists in a more optimum way, starting with what was known last fall as the Research Commitment Index. That effort, known temporarily as RCI, later morphed into the Grant Support Index, or GSI.

"[GSI] created quite a lot of interest—not all of it positive—about as much as I've seen in a grants funding policy in 8 years," said Collins. "We did hear significant concerns about the validity of the index, and how it might discourage collaboration." It became

SEE ACD, PAGE 4

Bill Gates (l) talks global health at NIH, p. 12.

ALSO THIS ISSUE

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JUNGLE TRAVEL NOT REQUIRED

Daly Lecturer Describes 21st Century Drug Discovery

BY CARLA GARNETT

Just recently back from a trip to South Africa, where she had a "pretty scary" face-to-face with a deadly black mamba snake, Dr. Fiona Marshall had the perfect introduction to NIH's 2017 Daly lecture.

Renowned jungle explorer Dr. John W. Daly, the late NIDDK biochemist and pharmacologist for whom Marshall's talk was named, pioneered in natural product research.

In much of the last half of last century, he

SEE MARSHALL, PAGE 6

Dr. Fiona Marshall

Genetics, Evolutionary Biology Help Identify Rare Mendelian Disorders

BY DANA TALESNIK

If Charles Darwin had read the findings of Gregor Mendel, he might have saved himself a lot of grief. While Mendel was holed up in a monastery discovering hereditary traits by experimenting on pea plants, Darwin was struggling to prove his theories of natural selection and descent-with-modification.

"Darwin's big problem was that, with descent-with-modification, there was no theory of genetics, no knowledge of

SEE VALLE, PAGE 8

Dr. David Valle

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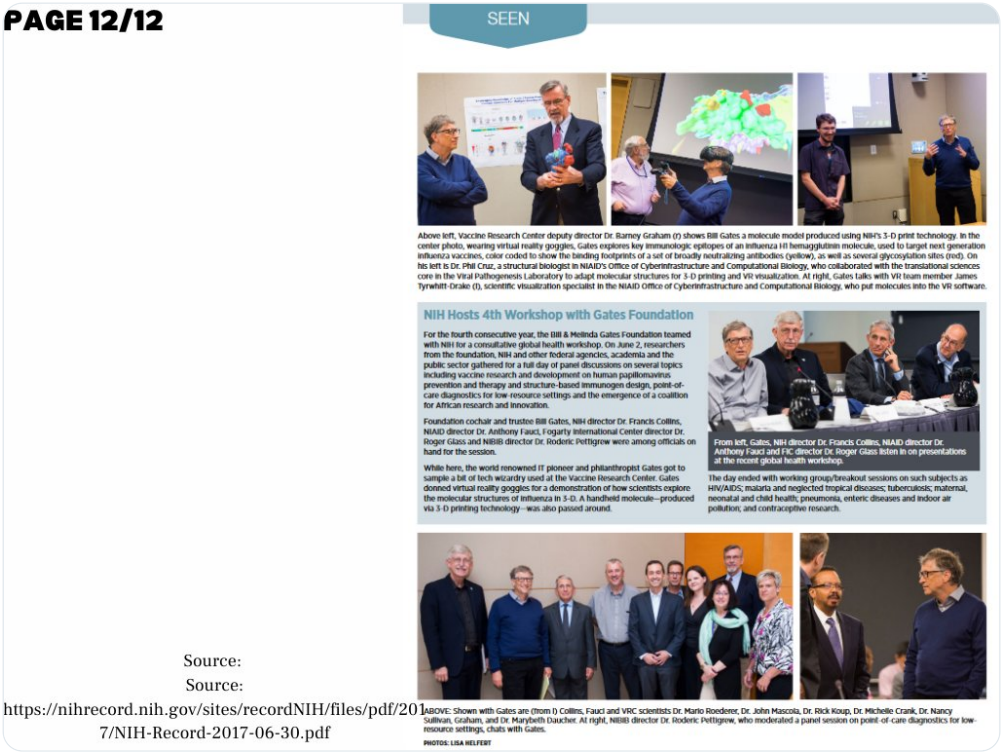
https://nihrecord.nih.gov/sites/recordNIH/files/pdf/201
7/NIH-Record-2017-06-30.pdf



PAGE 12/12

SEEN

Above left, Vaccine Research Center deputy director Dr. Barney Graham (r) shows Bill Gates a molecule model produced using NIH's 3-D print technology. In the center photo, wearing virtual reality goggles, Gates explores key immunologic epitopes of an influenza HI hemagglutinin molecule, used to target next generation influenza vaccines, color coded to show the binding footprints of a set of broadly neutralizing antibodies (yellow), as well as several glycosylation sites (red). On his left is Dr. Phil Cruz, a structural biologist in NIAID's Office of Cyberinfrastructure and Computational Biology, who collaborated with the translational sciences core in the Viral Pathogenesis Laboratory to adapt molecular structures for 3-D printing and VR visualization. At right, Gates talks with VR team member James Tyrwhitt-Drake (l), scientific visualization specialist in the NIAID Office of Cyberinfrastructure and Computational Biology, who put molecules into the VR software.

NIH Hosts 4th Workshop with Gates Foundation

For the fourth consecutive year, the Bill & Melinda Gates Foundation teamed with NIH for a consultative global health workshop. On June 2, researchers from the foundation, NIH and other federal agencies, academia and the public sector gathered for a full day of panel discussions on several topics including vaccine research and development on human papillomavirus prevention and therapy and structure-based immunogen design, point-of-care diagnostics for low-resource settings and the emergence of a coalition for African research and innovation.

Foundation cochair and trustee Bill Gates, NIH director Dr. Francis Collins, NIAID director Dr. Anthony Fauci, Fogarty International Center director Dr. Roger Glass and NIBIB director Dr. Roderic Pettigrew were among officials on hand for the session.

While here, the world renowned IT pioneer and philanthropist Gates got to sample a bit of tech wizardry used at the Vaccine Research Center. Gates donned virtual reality goggles for a demonstration of how scientists explore the molecular structures of influenza in 3-D. A handheld molecule—produced via 3-D printing technology—was also passed around.

From left, Gates, NIH director Dr. Francis Collins, NIAID director Dr. Anthony Fauci and FIC director Dr. Roger Glass listen in on presentations at the recent global health workshop.

The day ended with working group/breakout sessions on such subjects as HIV/AIDS; malaria and neglected tropical diseases; tuberculosis; maternal, neonatal and child health; pneumonia, enteric diseases and indoor air pollution; and contraceptive research.

ABOVE: Shown with Gates are (from l) Collins, Fauci and VRC scientists Dr. Mario Roederer, Dr. John Mascola, Dr. Rick Koup, Dr. Michelle Crank, Dr. Nancy Sullivan, Graham, and Dr. Marybeth Daucher. At right, NIBIB director Dr. Roderic Pettigrew, who moderated a panel session on point-of-care diagnostics for low-resource settings, chats with Gates.

PHOTOS: LISA HELFERT

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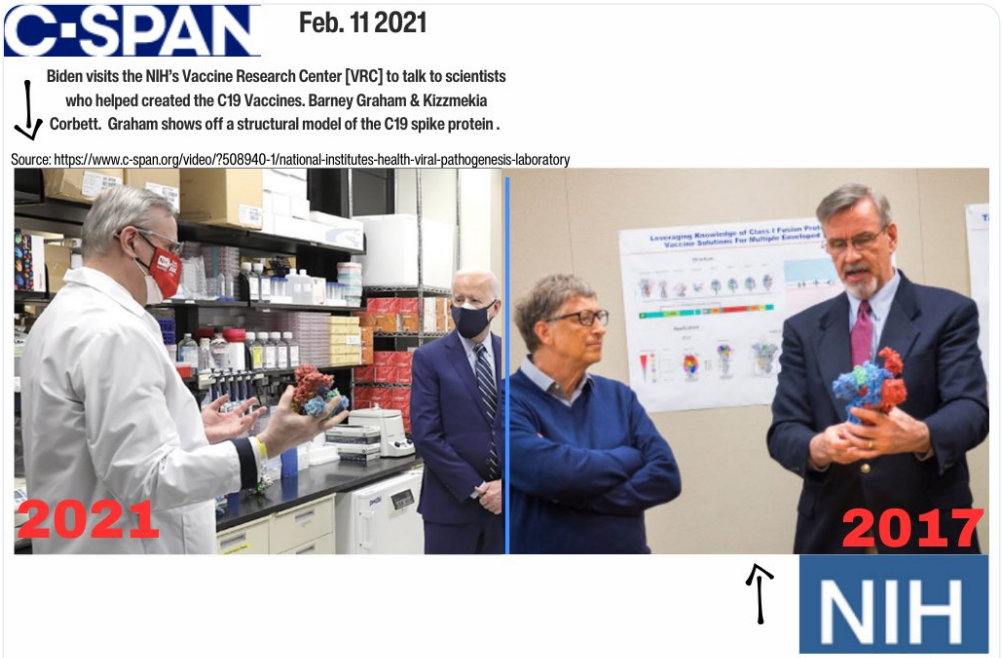
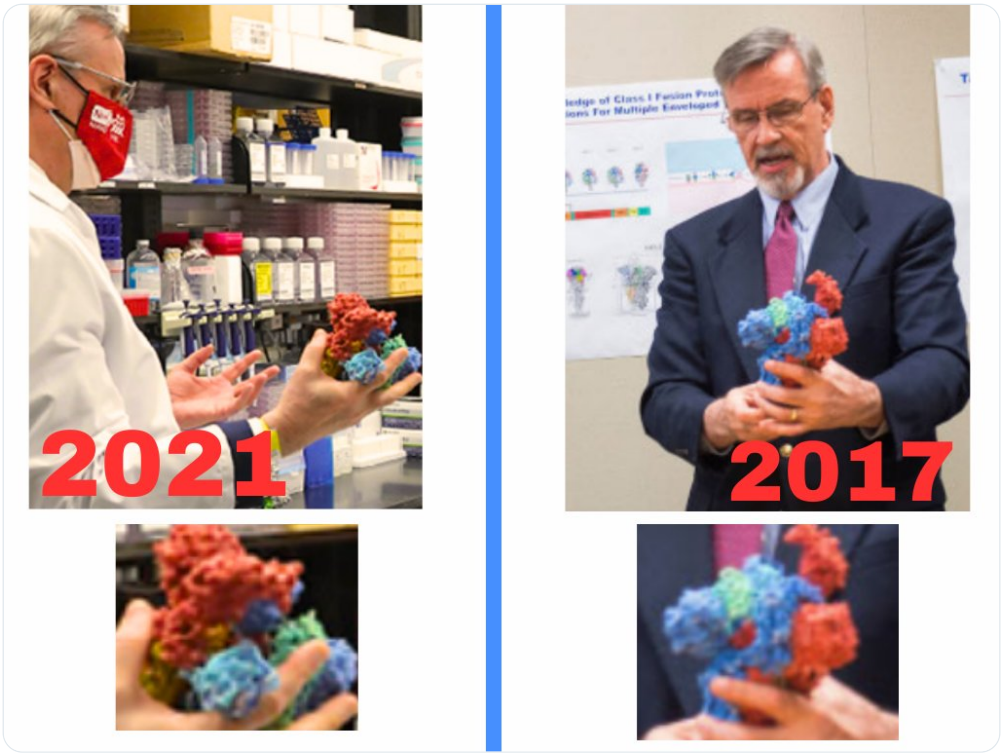
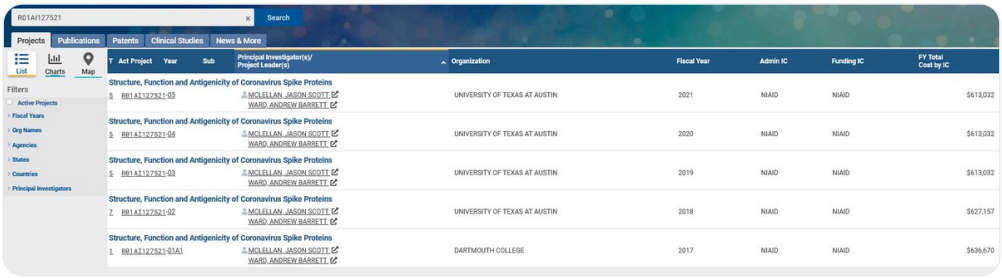
https://nihrecord.nih.gov/sites/recordNIH/files/pdf/201
7/NIH-Record-2017-06-30.pdf


C-SPAN
Feb. 11 2021
Biden visits the NIH's Vaccine Research Center [VRC] to talk to scientists who helped created the C19 Vaccines. Barney Graham & Kizzmekia Corbett. Graham shows off a structural model of the C19 spike protein .
Source: https://www.c-span.org/video/?508940-1/national-institutes-health-viral-pathogenesis-laboratory
2021
2017
NIH

Bill Gates & Barney Graham in 2017 for the annual meeting between Gate and NIH/NIAID/HHS,



3🧵On Feb 09 2017 The NIH began a grant round titled: "Structure, Function & Antigenicity of Coronavirus Spike Proteins" led by McLellan & Ward out of Dartmouth. The grant # is R01AI127521 & went 5 grant cycles from 2017-2021.


R01AI127521
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Structure, Function and Antigenicity of Coronavirus Spike Proteins
5 R01AI127521-05 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT UNIVERSITY OF TEXAS AT AUSTIN 2021 NIAID NIAID $613,032
Structure, Function and Antigenicity of Coronavirus Spike Proteins
5 R01AI127521-04 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT UNIVERSITY OF TEXAS AT AUSTIN 2020 NIAID NIAID $613,032
Structure, Function and Antigenicity of Coronavirus Spike Proteins
5 R01AI127521-03 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT UNIVERSITY OF TEXAS AT AUSTIN 2019 NIAID NIAID $613,032
Structure, Function and Antigenicity of Coronavirus Spike Proteins
7 R01AI127521-02 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT UNIVERSITY OF TEXAS AT AUSTIN 2018 NIAID NIAID $627,157
Structure, Function and Antigenicity of Coronavirus Spike Proteins
1 R01AI127521-01A1 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT DARTMOUTH COLLEGE 2017 NIAID NIAID $636,670

Agency	National Institute of Health (NIH)	**Project Start**	2017-02-09
Institute	National Institute of Allergy and Infectious Diseases (NIAID)	**Project End**	2022-01-31
		Budget Start	2017-02-09
Type	Research Project (R01)	**Budget End**	2018-01-31
Project #	1R01AI127521-01A1	**Support Year**	1
Application #	9328799	**Fiscal Year**	2017
Study Section	Virology - A Study Section (VIRA)	**Total Cost**	$636,670
		Indirect Cost	$124,349
Program Officer	Stemmy, Erik J		

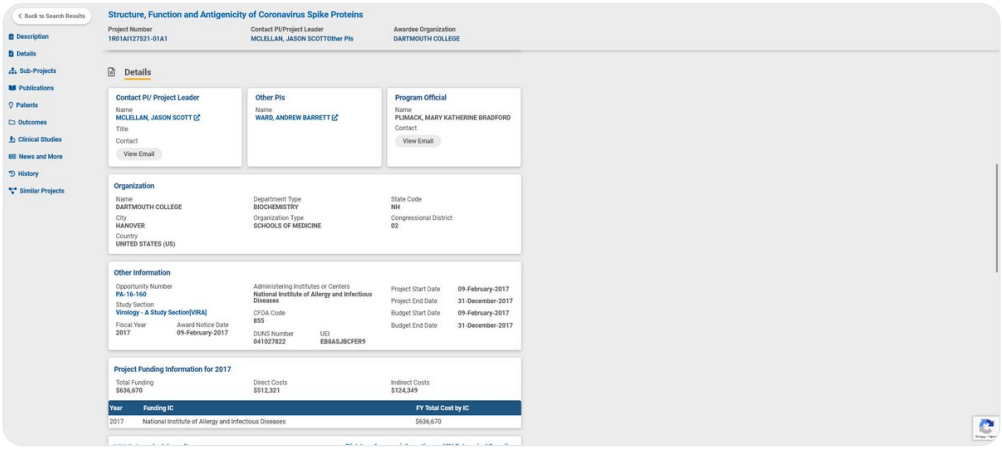
Institution

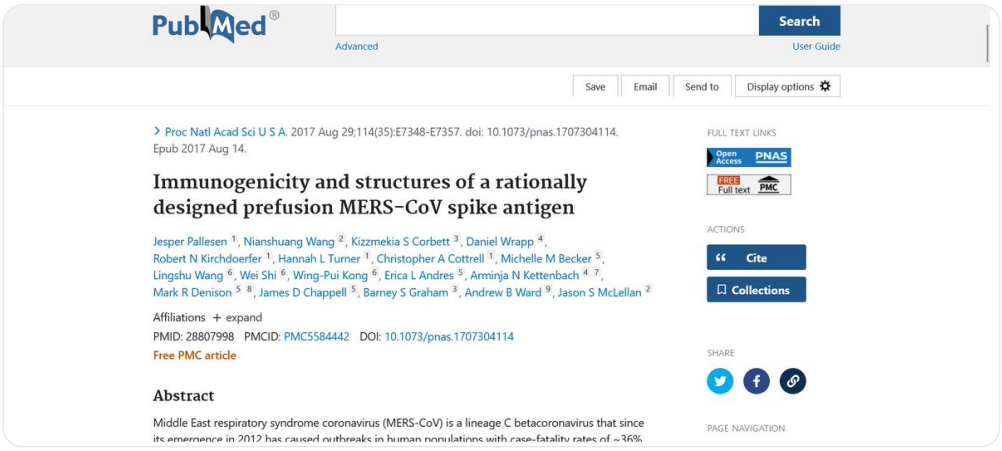
Name	Dartmouth College	**City**	Hanover
Department	Biochemistry	**State**	NH
Type	Schools of Medicine	**Country**	United States
DUNS #	041027822	**Zip Code**	03755

NIH 2021 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2020 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2019 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2018 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2017 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / Dartmouth College	$636,670

Yes, both Doctors Jason McLellan and Andrew Ward are associated with Dartmouth College. Jason McLellan is a professor of molecular biosciences at The University of Texas in Austin, and his lab is located at Dartmouth College in New Hampshire [3]. Andrew Ward is also linked to Dartmouth College, as a collaboration between Jason McLellan's group at Dartmouth and Andrew Ward's group took place in 2017, just three years before the emergence of SARS-CoV-2 [5].

4🧵W/in the NIH grant rounds under R01AI127521 a publication was funded. That paper, "Immunogenicity & structures of a rationally designed prefusion MERS-CoV spike antigen" was authored by not only Graham, Ward + McLellan but also Corbett & Denison👀

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Proc Natl Acad Sci U S A. 2017 Aug 29;114(35):E7348-E7357. doi: 10.1073/pnas.1707304114. Epub 2017 Aug 14.
Immunogenicity and structures of a rationally designed prefusion MERS-CoV spike antigen
Jesper Pallesen, Nianshuang Wang, Kizzmekia S Corbett, Daniel Wrapp, Robert N Kirchdoerfer, Hannah L Turner, Christopher A Cottrell, Michelle M Becker, Lingshu Wang, Wei Shi, Wing-Pui Kong, Erica L Andres, Arminja N Kettenbach, Mark R Denison, James D Chappell, Barney S Graham, Andrew B Ward, Jason S McLellan
Affiliations + expand
PMID: 28807998 PMCID: PMC5584442 DOI: 10.1073/pnas.1707304114
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Abstract
Middle East respiratory syndrome coronavirus (MERS-CoV) is a lineage C betacoronavirus that since
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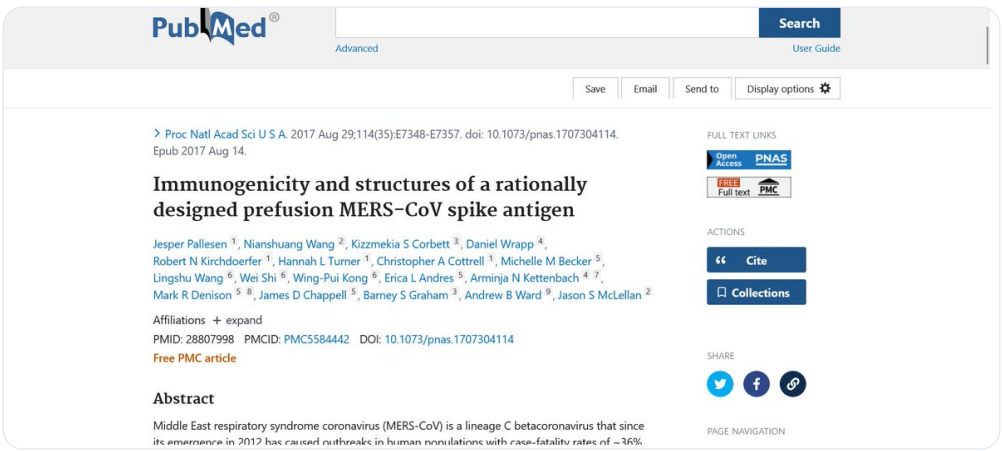
Agency	National Institute of Health (NIH)	**Project Start**	2017-02-09
Institute	National Institute of Allergy and Infectious Diseases (NIAID)	**Project End**	2022-01-31
		Budget Start	2017-02-09
Type	Research Project (R01)	**Budget End**	2018-01-31
Project #	1R01AI127521-01A1	**Support Year**	1
Application #	9328799	**Fiscal Year**	2017
Study Section	Virology - A Study Section (VIRA)	**Total Cost**	$636,670
		Indirect Cost	$124,349
Program Officer	Stemmy, Erik J		

Institution

Name	Dartmouth College	**City**	Hanover
Department	Biochemistry	**State**	NH
Type	Schools of Medicine	**Country**	United States
DUNS #	041027822	**Zip Code**	03755

NIH 2021 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2020 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2019 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2018 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / University of Texas Austin	
NIH 2017 R01 AI	Structure, Function and Antigenicity of Coronavirus Spike Proteins McLellan, Jason Scott; Ward, Andrew Barrett / Dartmouth College	$636,670

5🧵Corbett was the young black female scientist at the VRC in that 2021 video w/ Biden & Graham. She happens to be an understudy of Ralph Baric, graduate of UNC Chapel Hill. Denison was the top collab of Baric's during 2014-2020 from Vanderbilt.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Proc Natl Acad Sci U S A. 2017 Aug 29;114(35):E7348-E7357. doi: 10.1073/pnas.1707304114. Epub 2017 Aug 14.
Immunogenicity and structures of a rationally designed prefusion MERS-CoV spike antigen
Jesper Pallesen [1], Nianshuang Wang [2], Kizzmekia S Corbett [3], Daniel Wrapp [4], Robert N Kirchdoerfer [1], Hannah L Turner [1], Christopher A Cottrell [1], Michelle M Becker [5], Lingshu Wang [6], Wei Shi [6], Wing-Pui Kong [6], Erica L Andres [5], Arminja N Kettenbach [4 7], Mark R Denison [5 8], James D Chappell [5], Barney S Graham [3], Andrew B Ward [9], Jason S McLellan [2]
Affiliations + expand
PMID: 28807998 PMCID: PMC5584442 DOI: 10.1073/pnas.1707304114
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Abstract
Middle East respiratory syndrome coronavirus (MERS-CoV) is a lineage C betacoronavirus that since
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Source: https://news.vanderbilt.edu/2021/03/17/shot-in-the-arm-groundbreaking-covid-19-vaccine-research-by-alumnus-dr-barney-graham-began-at-vanderbilt-decades-ago/

CORONAVIRUS BREAKTHROUGH

Wright, Graham, Neuzil and Denison formed the nucleus of a unique community, which also included Dr. Kathryn Edwards and Dr. Bill Gruber. Edwards is now the Sarah H. Sell and Cornelius Vanderbilt Professor of Pediatrics at the School of Medicine. Gruber, who had been Graham's roommate at Rice and had come to Vanderbilt to work on vaccine trials for several viral diseases affecting children, is now the senior vice president of vaccine clinical research and development at Pfizer.

The group was unusually collaborative—Graham and Neuzil were adult physicians working on a childhood disease, while Wright, Edwards and Gruber were pediatricians running trials on an adult vaccine. Graham became the bridge among the various disciplines of adult and childhood diseases, as well as the basic science and clinical research.

By early 2020, Graham's group had designed the vaccine, and Moderna was ready to manufacture the Nipah mRNA and take it into a human clinical trial. But on Jan. 6, 2020, word came that Chinese scientists had isolated the virus that had caused an epidemic in Wuhan and was now in danger of creating a deadly worldwide pandemic.

"I called Jason and said, 'Get back in the saddle,'" Graham remembers. "'We're going to have to solve another structure.'"

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By now, the first cases of COVID-19 had emerged in the United States, adding new urgency to their mission. Graham collaborated with another group at NIH from the Division of Microbiology and Infectious Diseases that arranged to test the vaccine in humans just as the first animal data began showing efficacy. Neuzil worked with the team to design a trial of the first eight subjects in Seattle on March 16, followed shortly by another 37.

Usually it takes anywhere from 18 months to three years to develop a vaccine that can be used in people. In this instance, it took just a few weeks.

"Within 41 days after we gave Moderna the protein sequence, they gave us back an mRNA product that could be put into people," Graham says proudly. "We did animal and human studies in parallel, at the same time, so we would always have the data we needed to start the next stage."

Source: https://news.vanderbilt.edu/2021/03/17/shot-in-the-arm-groundbreaking-covid-19-vaccine-research-by-alumnus-dr-barney-graham-began-at-vanderbilt-decades-ago/

6🧵Two months after the "...prefusion MERS-CoV spike antigen" article a patent was issued on Oct 25 2017 titled: "PREFUSION CORONAVIRUS SPIKE PROTEINS AND THEIR USE" credited to HHS, Scripps and Dartmouth w/ Ward, McLellan, Graham & Corbett. This patent is credited 4 the C19 💉

JUSTIA Patents

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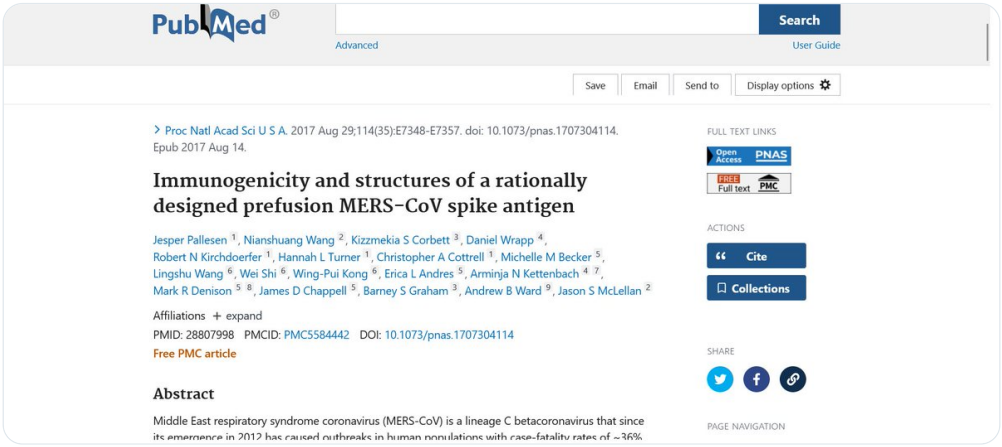
Patent History

Publication number: 20200061185
Type: Application
Filed: Oct 25, 2017
Publication Date: Feb 27, 2020
Patent Grant number: 10960070
Applicants: The United States of America, as represented by the Secretary, Department of Health and Human Servic (Bethesda, MD), The Scripps Research Institute (La Jolla, CA), Trustees of Dartmouth College (Hanover, NH)
Inventors: Barney Graham (Rockville, MD), Jason McLellan (Austin, TX), Andrew Ward (La Jolla, CA), Robert Kirchdoerfer (La Jolla, CA), Christopher Cottrell (La Jolla, CA), Michael Gordon Joyce (Washington, DC), Masaru Kanekiyo (Chevy Chase, MD), Nianshuang Wang (Hanover, NH), Jesper Pallesen (La Jolla, CA), Hadi Yassine (Doha), Hannah Turner (La Jolla, CA), Kizzmekia Corbett (Bethesda, MD)
Application Number: 16/344,774

Classifications

International Classification: A61K 39/215 (20060101); C07K 14/005 (20060101); A61P 31/14 (20060101); C12N 7/00 (20060101);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Proc Natl Acad Sci U S A. 2017 Aug 29;114(35):E7348-E7357. doi: 10.1073/pnas.1707304114. Epub 2017 Aug 14.
Immunogenicity and structures of a rationally designed prefusion MERS-CoV spike antigen
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Affiliations + expand
PMID: 28807998 PMCID: PMC5584442 DOI: 10.1073/pnas.1707304114
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Abstract
Middle East respiratory syndrome coronavirus (MERS-CoV) is a lineage C betacoronavirus that since its emergence in 2012 has caused outbreaks in human populations with case-fatality rates of ~36%
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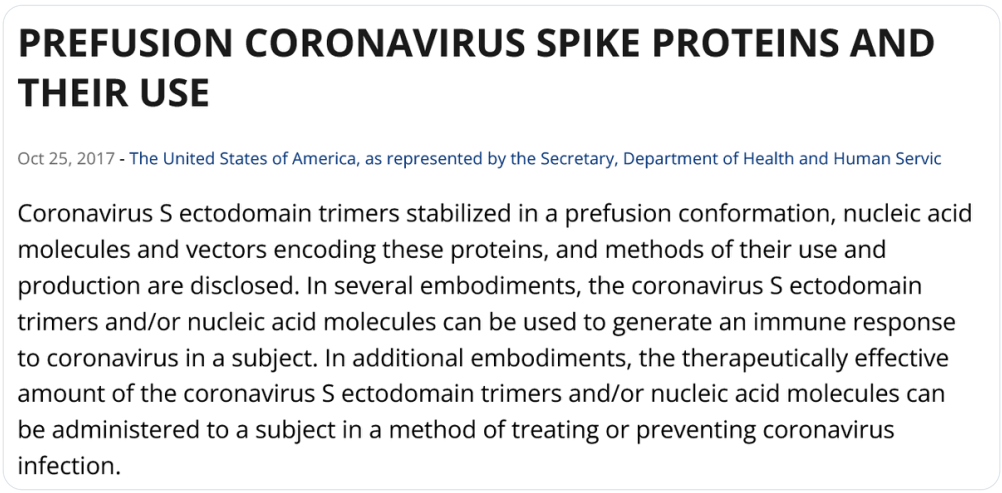
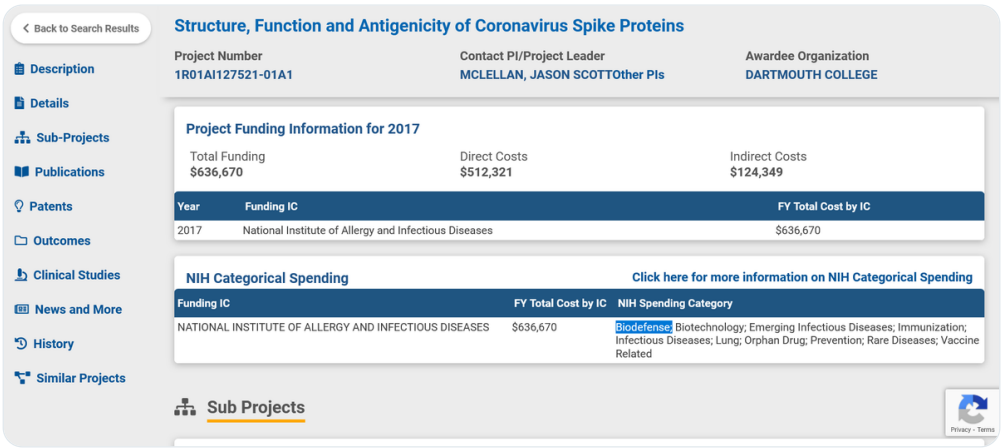
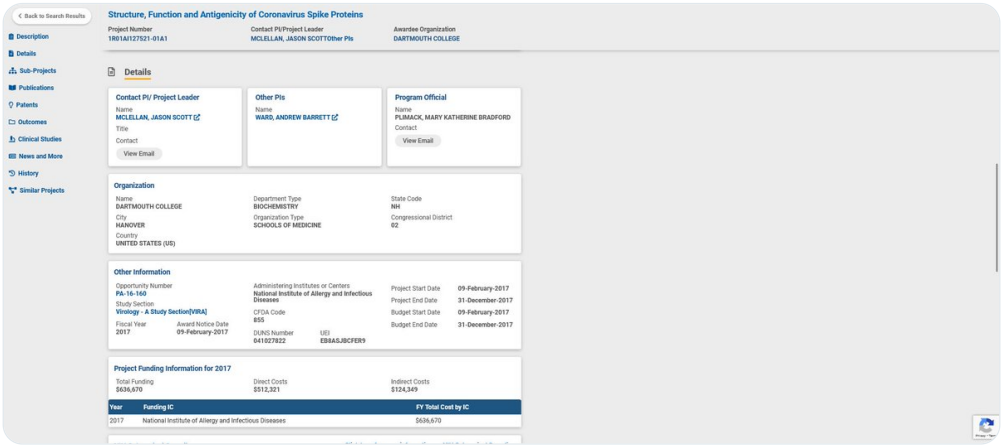
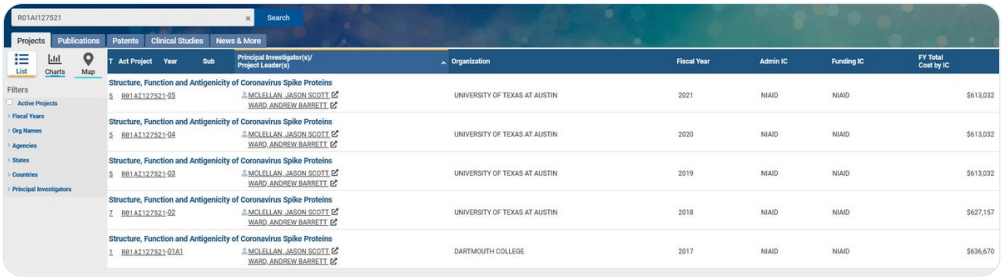

PREFUSION CORONAVIRUS SPIKE PROTEINS AND THEIR USE
Oct 25, 2017 - The United States of America, as represented by the Secretary, Department of Health and Human Servic
Coronavirus S ectodomain trimers stabilized in a prefusion conformation, nucleic acid molecules and vectors encoding these proteins, and methods of their use and production are disclosed. In several embodiments, the coronavirus S ectodomain trimers and/or nucleic acid molecules can be used to generate an immune response to coronavirus in a subject. In additional embodiments, the therapeutically effective amount of the coronavirus S ectodomain trimers and/or nucleic acid molecules can be administered to a subject in a method of treating or preventing coronavirus infection.

7🧵Two things that surprised me was; #1 the classification of the research under grant R01AI127521 which according to the NIH's grant repository RePORTER was listed as "Biodefense"



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Structure, Function and Antigenicity of Coronavirus Spike Proteins
5 R01AI127521-05 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT UNIVERSITY OF TEXAS AT AUSTIN 2021 NIAID NIAID $613,032
Structure, Function and Antigenicity of Coronavirus Spike Proteins
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5 R01AI127521-03 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT UNIVERSITY OF TEXAS AT AUSTIN 2019 NIAID NIAID $613,032
Structure, Function and Antigenicity of Coronavirus Spike Proteins
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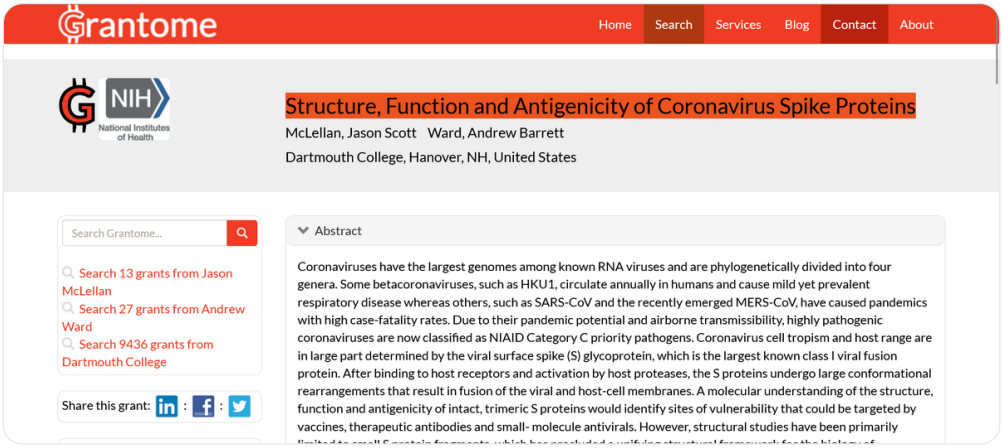
Structure, Function and Antigenicity of Coronavirus Spike Proteins
1 R01AI127521-01A1 MCLELLAN, JASON SCOTT WARD, ANDREW BARRETT DARTMOUTH COLLEGE 2017 NIAID NIAID $636,670

8🧵#2- If you were to type the 2017 grant title "Structure, Function & Antigenicity of Coronavirus Spike Proteins" into NIH's Pubmed you get a paper titled "Structure, Function, and Evolution of Coronavirus Spike Proteins" from Sept 29 2016. The titles are one word off...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Structure, Function and Antigenicity of Coronavirus Spike Proteins
McLellan, Jason Scott Ward, Andrew Barrett
Dartmouth College, Hanover, NH, United States
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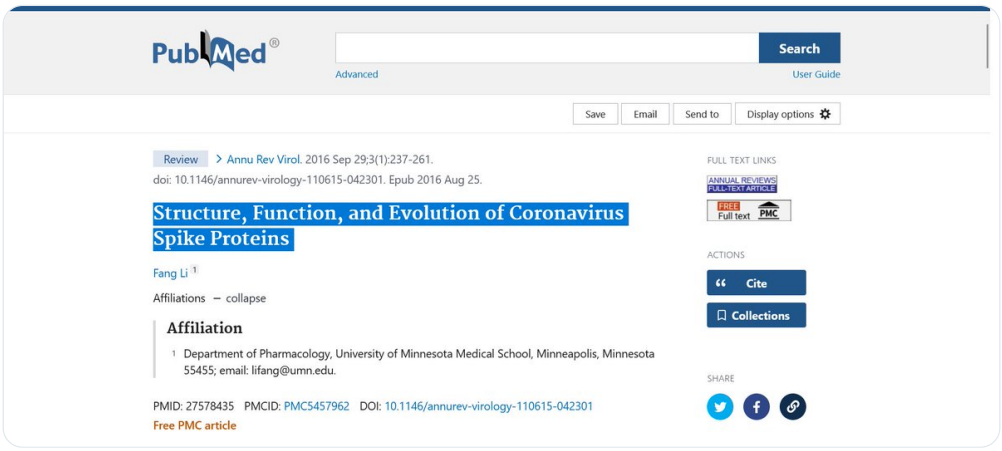
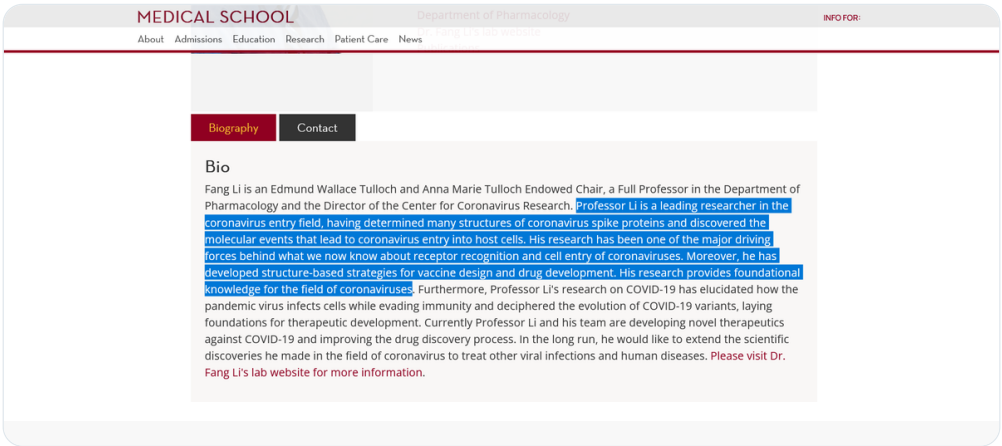
Abstract
Coronaviruses have the largest genomes among known RNA viruses and are phylogenetically divided into four genera. Some betacoronaviruses, such as HKU1, circulate annually in humans and cause mild yet prevalent respiratory disease whereas others, such as SARS-CoV and the recently emerged MERS-CoV, have caused pandemics with high case-fatality rates. Due to their pandemic potential and airborne transmissibility, highly pathogenic coronaviruses are now classified as NIAID Category C priority pathogens. Coronavirus cell tropism and host range are in large part determined by the viral surface spike (S) glycoprotein, which is the largest known class I viral fusion protein. After binding to host receptors and activation by host proteases, the S proteins undergo large conformational rearrangements that result in fusion of the viral and host-cell membranes. A molecular understanding of the structure, function and antigenicity of intact, trimeric S proteins would identify sites of vulnerability that could be targeted by vaccines, therapeutic antibodies and small- molecule antivirals. However, structural studies have been primarily



9🧵One word off but NONE of the same Authors. The 2016 paper is written solely by Fang-Li of Univ. Minn. The paper isn't even funded by the same grant [R01AI127521] but it is funded by grants AI110700, & AI089728. Both grants are to Fang-Li for CoV research.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Department of Pharmacology
Fang Li's lab website
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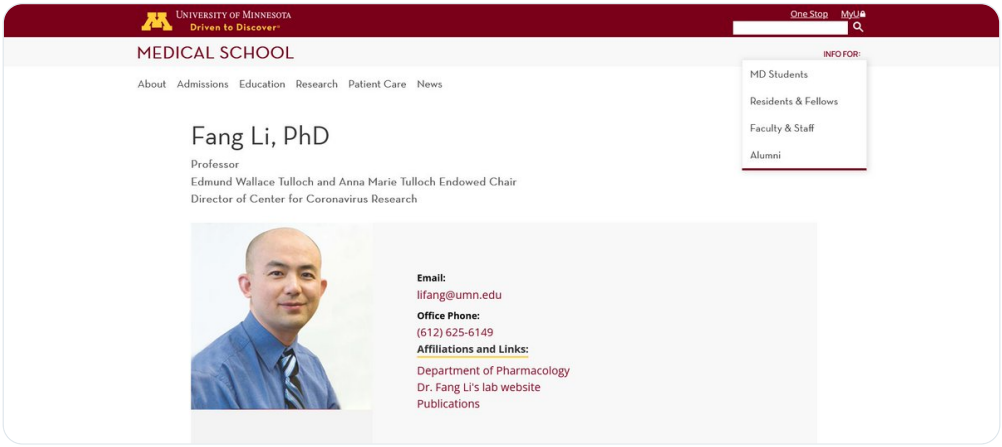
Bio
Fang Li is an Edmund Wallace Tulloch and Anna Marie Tulloch Endowed Chair, a Full Professor in the Department of Pharmacology and the Director of the Center for Coronavirus Research. Professor Li is a leading researcher in the coronavirus entry field, having determined many structures of coronavirus spike proteins and discovered the molecular events that lead to coronavirus entry into host cells. His research has been one of the major driving forces behind what we now know about receptor recognition and cell entry of coronaviruses. Moreover, he has developed structure-based strategies for vaccine design and drug development. His research provides foundational knowledge for the field of coronaviruses. Furthermore, Professor Li's research on COVID-19 has elucidated how the pandemic virus infects cells while evading immunity and deciphered the evolution of COVID-19 variants, laying foundations for therapeutic development. Currently Professor Li and his team are developing novel therapeutics against COVID-19 and improving the drug discovery process. In the long run, he would like to extend the scientific discoveries he made in the field of coronavirus to treat other viral infections and human diseases. Please visit Dr. Fang Li's lab website for more information.



Review > Annu Rev Virol. 2016 Sep 29;3(1):237-261.
doi: 10.1146/annurev-virology-110615-042301. Epub 2016 Aug 25.

Structure, Function, and Evolution of Coronavirus Spike Proteins

Fang Li [1]

Affiliations – collapse

Affiliation

1 Department of Pharmacology, University of Minnesota Medical School, Minneapolis, Minnesota 55455; email: lifang@umn.edu.

PMID: 27578435 PMCID: PMC5457962 DOI: 10.1146/annurev-virology-110615-042301
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Substances

> Membrane Glycoproteins
> Receptors, Virus
> Spike Glycoprotein, Coronavirus
> Viral Envelope Proteins

Related information

Domains
MedGen
PMC images

Grants and funding

R01 AI089728/AI/NIAID NIH HHS/United States
R01 AI110700/AI/NIAID NIH HHS/United States

10 🧵 One of those NIH grants [AI110700] was co-led by none other than Ralph Baric. Again, same titled research, which led to the patent for C19 💉's but hidden under different grants,

even though the 💉patent is used by Moderna which Baric already signed an MTA w/ <1yr later 🤔

Review > Annu Rev Virol. 2016 Sep 29;3(1):237-261.
doi: 10.1146/annurev-virology-110615-042301. Epub 2016 Aug 25.

Structure, Function, and Evolution of Coronavirus Spike Proteins

Fang Li [1]

Affiliations – collapse

Affiliation

1 Department of Pharmacology, University of Minnesota Medical School, Minneapolis, Minnesota 55455; email: lifang@umn.edu.

PMID: 27578435 PMCID: PMC5457962 DOI: 10.1146/annurev-virology-110615-042301
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Substances

> Membrane Glycoproteins
> Receptors, Virus
> Spike Glycoprotein, Coronavirus
> Viral Envelope Proteins

Related information

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MedGen
PMC images

Grants and funding

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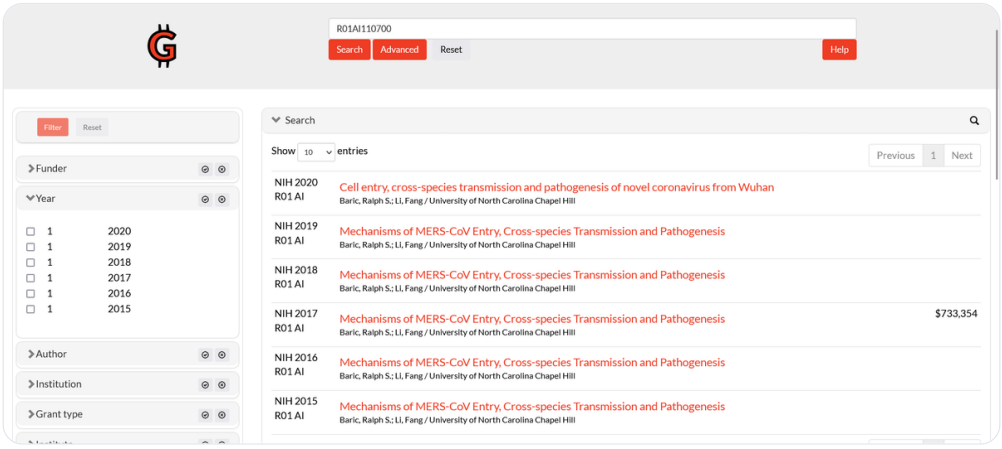
R01 AI110700/AI/NIAID NIH HHS/United States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Cell entry, cross-species transmission and pathogenesis of novel coronavirus from Wuhan
Baric, Ralph S.; Li, Fang / University of North Carolina Chapel Hill
NIH 2019 R01 AI
Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis
Baric, Ralph S.; Li, Fang / University of North Carolina Chapel Hill
NIH 2018 R01 AI
Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis
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Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis
Baric, Ralph S.; Li, Fang / University of North Carolina Chapel Hill
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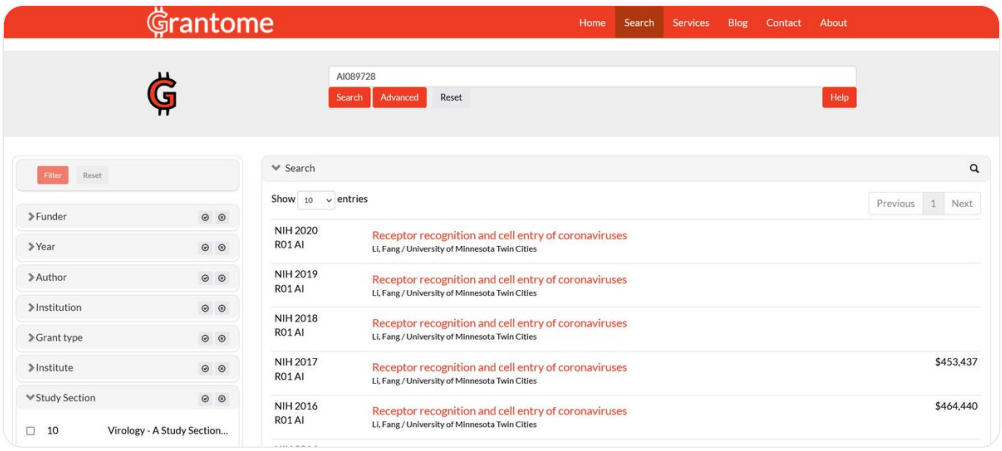

11🧵If Fang-Li sounds familiar it's likely because he has worked significantly with Baric & Zheng-Li Shi & Eco Health Alliance on Coronaviruses & now is the Director, Center for Coronavirus Research😳

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Discovery of Novel Bat Coronaviruses in South China That Use the Same Receptor as Middle East Respiratory Syndrome Coronavirus

Chu-Ming Luo,[a,b,c] Ning Wang,[a,b] Xing-Lou Yang,[a] Hai-Zhou Liu,[a] Wei Zhang,[a] Bei Li,[a] Ben Hu,[a] Cheng Peng,[a] Qi-Bin Geng,[c] Guang-Jian Zhu,[d] Fang Li,[c] Zheng-Li Shi[a]

[a]CAS Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China
[b]University of Chinese Academy of Sciences, Beijing, China
[c]Department of Veterinary and Biomedical Sciences, University of Minnesota, Saint Paul, Minnesota, USA
[d]EcoHealth Alliance, New York, New York, USA

ABSTRACT Middle East respiratory syndrome coronavirus (MERS-CoV) has represented a human health threat since 2012. Although several MERS-related CoVs that

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[a]CAS Key Laboratory of Special Pathogens and Biosafety, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei, China
[b]University of Chinese Academy of Sciences, Beijing, China
[c]Department of Veterinary and Biomedical Sciences, University of Minnesota, Saint Paul, Minnesota, USA
[d]EcoHealth Alliance, New York, New York, USA

ABSTRACT Middle East respiratory syndrome coronavirus (MERS-CoV) has represented a human health threat since 2012. Although several MERS-related CoVs that belong to the same species as MERS-CoV have been identified from bats, they do not use the MERS-CoV receptor, dipeptidyl peptidase 4 (DPP4). Here, we screened 1,059 bat samples from at least 30 bat species collected in different regions in south China and identified 89 strains of lineage C betacoronaviruses, including *Tylonycteris pachypus coronavirus HKU4*, *Pipistrellus pipistrellus coronavirus HKU5*, and MERS-related CoVs. We sequenced the full-length genomes of two positive samples collected from the great evening bat, *Ia io*, from Guangdong Province. The two genomes were highly similar and exhibited genomic structures identical to those of other lineage C betacoronaviruses. While they exhibited genome-wide nucleotide identities of only 75.3 to 81.2% with other MERS-related CoVs, their gene-coding regions were highly similar to their counterparts, except in the case of the spike proteins. Further protein-protein interaction assays demonstrated that the spike proteins of these MERS-related CoVs bind to the receptor DPP4. Recombination analysis suggested that the newly discovered MERS-related CoVs have acquired their spike genes from a DPP4-recognizing bat coronavirus HKU4. Our study provides further evidence that bats represent the evolutionary origins of MERS-CoV.

IMPORTANCE Previous studies suggested that MERS-CoV originated in bats. However, its evolutionary path from bats to humans remains unclear. In this study, we discovered 89 novel lineage C betacoronaviruses in eight bat species. We provide evidence of a MERS-related CoV derived from the great evening bat that uses the same host receptor as human MERS-CoV. This virus also provides evidence for a natural recombination event between the bat MERS-related CoV and another bat coronavirus, HKU4. Our study expands the host ranges of MERS-related CoV and represents an important step toward establishing bats as the natural reservoir of MERS-CoV. These findings may lead to improved epidemiological surveillance of MERS-CoV and the prevention and control of the spread of MERS-CoV to humans.

KEYWORDS MERS-related coronavirus, bat, dipeptidyl peptidase 4, virus discovery

Coronaviruses (CoVs) infect a wide range of mammalian and avian hosts, causing respiratory, enteric, hepatic, or neurological diseases of varying severity. These viruses have the largest genomes among all RNA viruses, leading to an increased number of replication errors compared to the host genome (1). Different CoVs can also recombine their genomes upon infecting the same host cell, contributing substantially

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Editor Tom Gallagher, Loyola University Medical Center
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Address correspondence to Fang Li, lifang@umn.edu, or Zheng-Li Shi, zlshi@wh.iov.cn.

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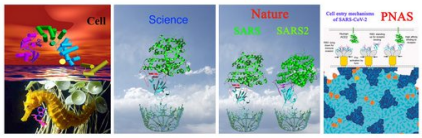


Resume, Research, Publications, Awards, News, CCR

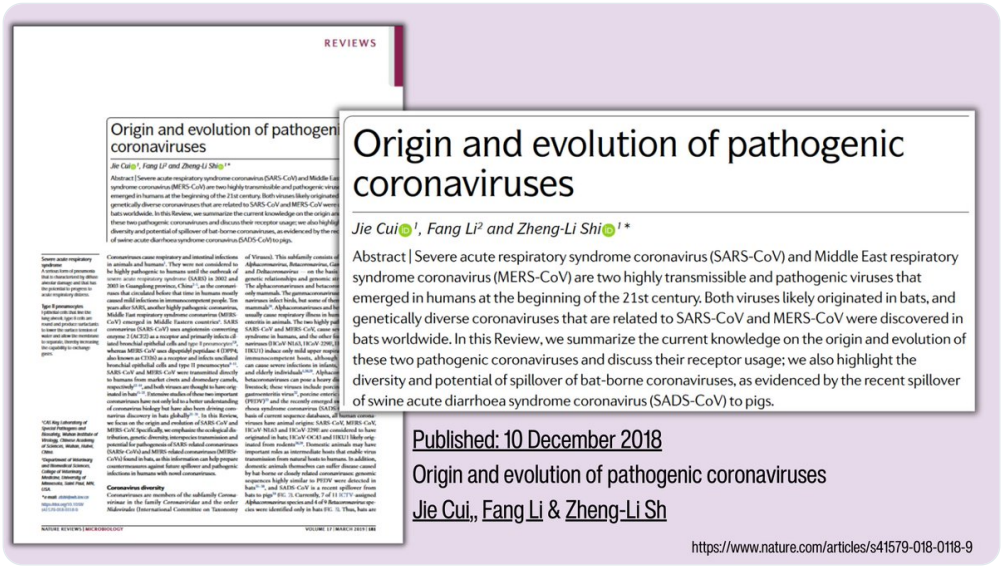
Fang Li, PhD

Professor and Endowed Chair, Deparment of Pharmacology

Director, Center for Coronavirus Research

Co-Director, Midwest Antiviral Drug Discovery Center

University of Minnesota Medical School


REVIEWS
Origin and evolution of pathogenic coronaviruses
Origin and evolution of pathogenic coronaviruses
Jie Cui[1], Fang Li[2] and Zheng-Li Shi[1]*
Abstract | Severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) are two highly transmissible and pathogenic viruses that emerged in humans at the beginning of the 21st century. Both viruses likely originated in bats, and genetically diverse coronaviruses that are related to SARS-CoV and MERS-CoV were discovered in bats worldwide. In this Review, we summarize the current knowledge on the origin and evolution of these two pathogenic coronaviruses and discuss their receptor usage; we also highlight the diversity and potential of spillover of bat-borne coronaviruses, as evidenced by the recent spillover of swine acute diarrhoea syndrome coronavirus (SADS-CoV) to pigs.
Published: 10 December 2018
Origin and evolution of pathogenic coronaviruses
Jie Cui,, Fang Li & Zheng-Li Sh
https://www.nature.com/articles/s41579-018-0118-9

12🧵Coincidence? I think not. An attempt to hide the creation of certain GoF research turned bio-weapon? MUCH more likely. Stay tuned-I'm still not done 🔎👀🧾

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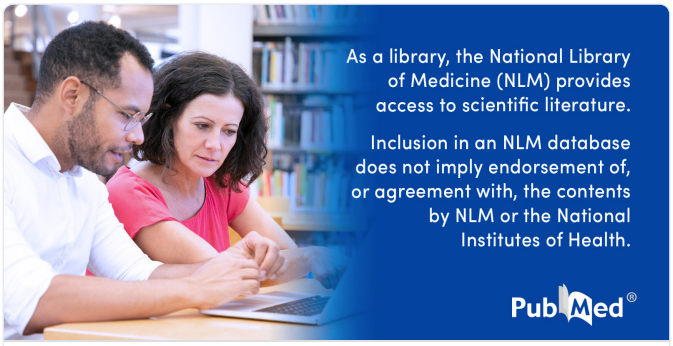
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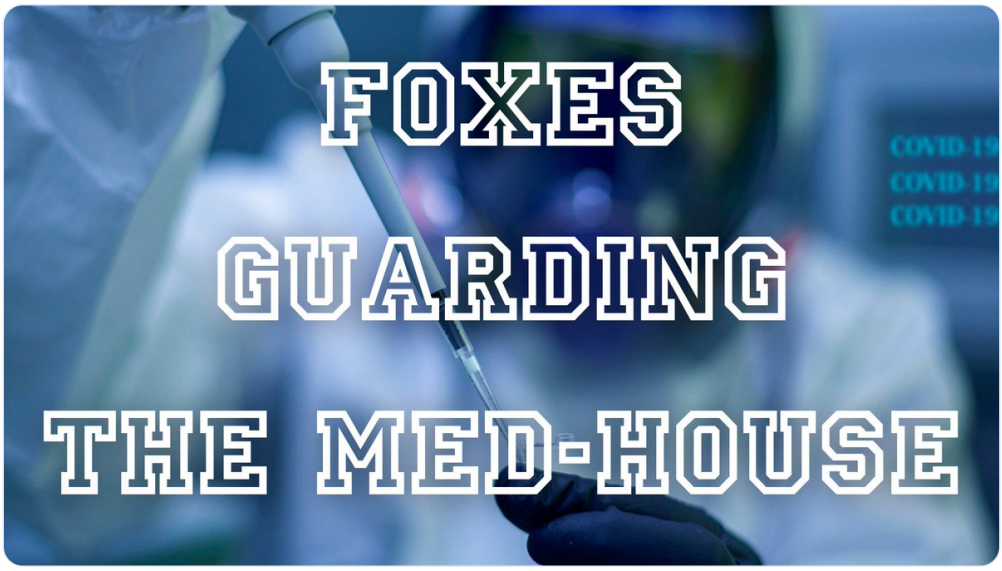
Destiny Rezendes @dezzie_rezzie

Dec 2, 2023 • 13 tweets • dezzie_rezzie/status/1731093081661772169

1🧵Continuing w/ my recent threads exposing the Conflicts of Interest [COI] in the oversight efforts & early investigations of the pandemic. I have more data to prove to you that this 'Scamdemic' is a certified rigged racket.



2🧵40 days after the C19 genome was made public a group of "concerned" scientists submitted a statement to stand in support of "the science" in Wuhan. Admonishing the "conspiracy theories" floating around of a lab leak. Published in the lancet, it is a certified fraud.

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Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19
Charles Calisher • Dennis Carroll • Rita Colwell • Ronald B Corley • Peter Daszak • Christian Drosten • Luis Enjuanes • Jeremy Farrar • Hume Field • Josie Golding • Alexander Gorbalenya • Bart Haagmans • James M Hughes • William B Karesh • Gerald T Keusch • Sai Kit Lam • Juan Lubroth • John S Mackenzie • Larry Madoff • Jonna Mazet • Peter Palese • Stanley Perlman • Leo Poon • Bernard Roizman • Linda Saif • Kanta Subbarao • Mike Turner • Show less
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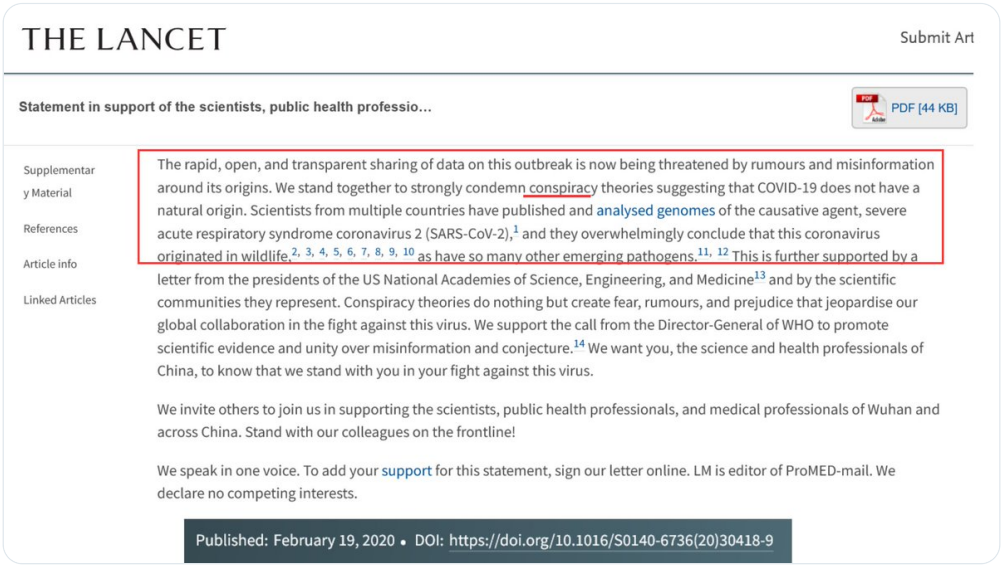
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The rapid, open, and transparent sharing of data on this outbreak is now being threatened by rumours and misinformation around its origins. We stand together to strongly condemn conspiracy theories suggesting that COVID-19 does not have a natural origin. Scientists from multiple countries have published and analysed genomes of the causative agent, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2),[1] and they overwhelmingly conclude that this coronavirus originated in wildlife,[2, 3, 4, 5, 6, 7, 8, 9, 10] as have so many other emerging pathogens.[11, 12] This is further supported by a letter from the presidents of the US National Academies of Science, Engineering, and Medicine[13] and by the scientific communities they represent. Conspiracy theories do nothing but create fear, rumours, and prejudice that jeopardise our global collaboration in the fight against this virus. We support the call from the Director-General of WHO to promote scientific evidence and unity over misinformation and conjecture.[14] We want you, the science and health professionals of China, to know that we stand with you in your fight against this virus.
We invite others to join us in supporting the scientists, public health professionals, and medical professionals of Wuhan and across China. Stand with our colleagues on the frontline!
We speak in one voice. To add your support for this statement, sign our letter online. LM is editor of ProMED-mail. We declare no competing interests.
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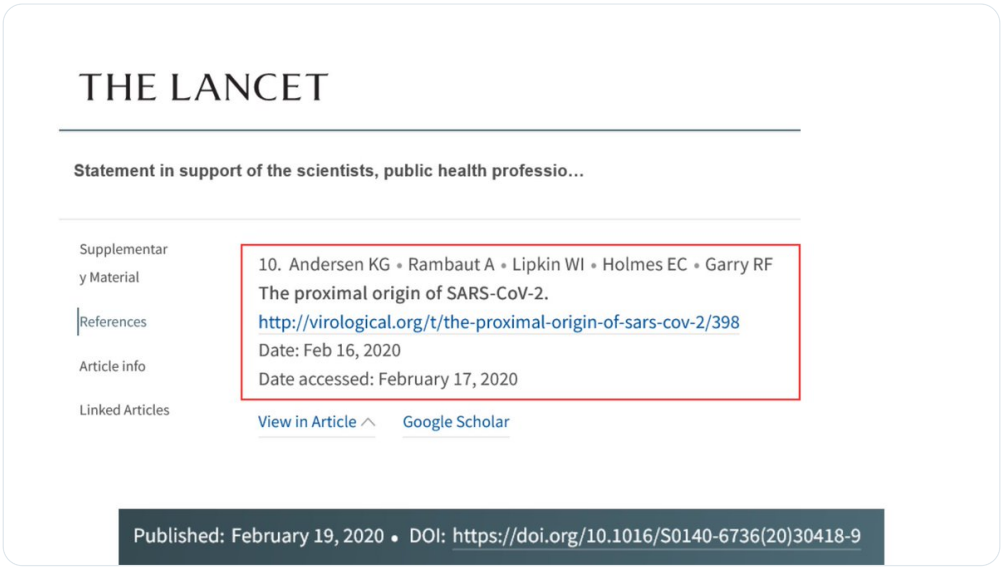
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Supplementary Material
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10. Andersen KG • Rambaut A • Lipkin WI • Holmes EC • Garry RF
The proximal origin of SARS-CoV-2.
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Google Scholar
Published: February 19, 2020 • DOI: https://doi.org/10.1016/S0140-6736(20)30418-9

3🧵The paper was signed by a slew of implicated characters; Dennis Carroll [ex USAID] & he is joined by fellow EHA heads Karesh, Mazet, Field, & Daszak. NIH cronies like Palese, Turner & Perlman. The Wellcome Trust poster child Jeremy Farrar & virologist Linda Saif 🤫

of 2019 novel coronavirus disease (COVID-19) and are deeply concerned about its impact on global health and wellbeing. We have watched as the scientists, public health professionals, and medical professionals of China, in particular, have worked diligently and effectively to rapidly identify the pathogen behind this outbreak, put in place significant measures to reduce its impact, and share their results transparently with the global health community. This effort has been remarkable.

We sign this statement in solidarity with all scientists and health professionals in China who continue to save lives and protect global health during the challenge of the COVID-19 outbreak. We are all in this together, with our Chinese counterparts in the forefront, against this new viral threat.

The rapid, open, and transparent

We invite others to join us in supporting the scientists, public health professionals, and medical professionals of Wuhan and across China. Stand with our colleagues on the frontline!

We speak in one voice. To add your support for this statement, sign our letter online. LM is editor of ProMED-mail. We declare no competing interests.

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COVID19statement@gmail.com

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Correspondence

Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19

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Colorado State University, Fort Collins, CO, USA (CC); Scowcroft Institute of International Affairs, Texas A&M, College Station, TX, USA (DC); University of Maryland, College Park, MD, USA (RC); NEIDL Institute (RBC), Boston University (GTC), Boston, MA, USA; EcoHealth Alliance, New York, NY, USA (PD); Charité – Universitatsmedizin Berlin, Berlin, Germany (CD); National Center of Biotechnology, Madrid, Spain (LE); The Wellcome Trust, London, UK (JF, JG, MT); School of Veterinary Science, The University of Queensland, Brisbane, QLD, Australia (HF); Leiden University Medical Center, Leiden, Netherlands (AG); Erasmus Medical Center, Rotterdam, Netherlands (BH); Emory University, Atlanta, GA, USA (JMH); World Organization for Animal Health (OIE) Working Group on Wildlife, New York, NY, USA (WBK); University of Malaya, Kuala Lumpur, Malaysia (SKL); Food and Agriculture Organization of the United Nations, Rome, Italy (JL); Curtin University, Perth, WA, Australia (JSMi); Massachusetts Medical School, Worcester, MA, USA (LM); University of California at Davis, Davis, CA, USA (JM); Department of Microbiology, Icahn School of Medicine, Mt Sinai Hospital, New York, NY, USA (PP); University of Iowa, Roy J and Lucille A Carver College of Medicine, Iowa City, IA, USA (SP); The University of Hong Kong, Hong Kong (LP), University of Chicago, Chigaco, IL, USA (BR); The Ohio State University, Columbus, OH, USA (LS); and The University of Melbourne, Melbourne, VIC, Australia (KS)

1 Gorbalenya AE, Baker SC, Baric RS, et al. Severe acute respiratory syndrome-related coronavirus: the species and its viruses—a statement of the Coronavirus Study Group. *bioRxiv* 2020; published online Feb 11. DOI:2020.02.07.937862 (preprint).

2 Zhou P, Yang X-L, Wang X-G, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020; published online Feb 3. DOI:10.1038/s41586-020-2012-7.

3 Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020; published online Jan 30. https://doi.org/10.1016/S0140-6736(20)30251-8.

4 Zhu N, Zhang D, Wang W, et al. A novel coronavirus from patients with pneumonia in China, 2019. *NEJM* 2020; published online Jan 24. DOI:10.1056/NEJMoa2001017.

5 Ren L, Wang Y-M, Wu Z-Q, et al. Identification of a novel coronavirus causing severe pneumonia in humans: a descriptive study. *Chin Med J* 2020; published online Feb 11. DOI:10.1097/CM9.0000000000000722.

6 Paraskevis D, Kostaki EG, Magiorkinis G, Panayiotakopoulos G, Splaidas S. Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event. *Infect Genet Evol* 2020; published online Jan 29. DOI:10.1016/j.meegid.2020.104212.

7 Benvenuto D, Giovanetti M, Ciccozzi A, Spoto S, Angeletti S, Ciccozzi M. The 2019-new coronavirus epidemic: evidence for virus evolution. *J Med Virol* 2020; published online Jan 29. DOI:10.1002/jmv.25688.

8 Wan Y, Shang J, Graham R, Baric RS, Li F. Receptor recognition by novel coronavirus from Wuhan: an analysis based on decade-long structural studies of SARS. *J Virol* 2020; published online Jan 29. DOI:10.1128/JVI.00127-20.

9 US Center for Disease Control and Prevention. Coronavirus disease 2019 (COVID-19) situation summary. Feb 16, 2020. https://www.cdc.gov/coronavirus/2019-nCoV/summary.html (accessed Feb 8, 2020).

10 Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. Feb 16, 2020. http://virological.org/t/the-proximal-origin-of-sars-cov-2/398 (accessed Feb 17, 2020).

11 Bengis R, Leighton F, Fischer J, Artois M, Morner T, Tate C. The role of wildlife in emerging and re-emerging zoonoses. *Rev Sci Tech* 2004; 23: 497–511.

12 Woolhouse ME, Gowtage-Sequeria S. Host range and emerging and reemerging pathogens. *Emerg Infect Dis* 2005; 11: 1842–47.

13 NASEM. The National Academies of Science Engineering and Medicine of the USA. NAS, NAE, and NAM presidents' letter to the White House Office of Science and Technology Policy. Feb 6, 2020. https://www.nationalacademies.org/includes/NASEMs%20Responses%20to%20STPs%20re%20Coronavirus_Februarys%206,%202020.pdf (accessed Feb 7, 2020).

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For the SARS-CoV-2 genome analysis see https://www.gisaid.org/epiflu-applications/next-betacov-app/

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4🧵The paper uses the CIA-Warren Commission Era tactic of tossing around the label of "conspiracy theorist" to ostracize those against the corrupt narrative. Ralph Baric is the first reference they cited & the Proximal Origins paper & WE are the conspiracy theorists?! 👀

Hong Kong, Hong Kong (LP); University of Chicago, Chigaco, IL, USA (BR); The Ohio State University, Columbus, OH, USA (LS); and The University of Melbourne, Melboune, VIC, Australia (KS)

1 Gorbalenya AE, Baker SC, Baric RS, et al. Severe acute respiratory syndrome-related coronavirus: the species and its viruses—a statement of the Coronavirus Study Group. *bioRxiv* 2020; published online Feb 11. DOI:2020.02.07.937862 (preprint).

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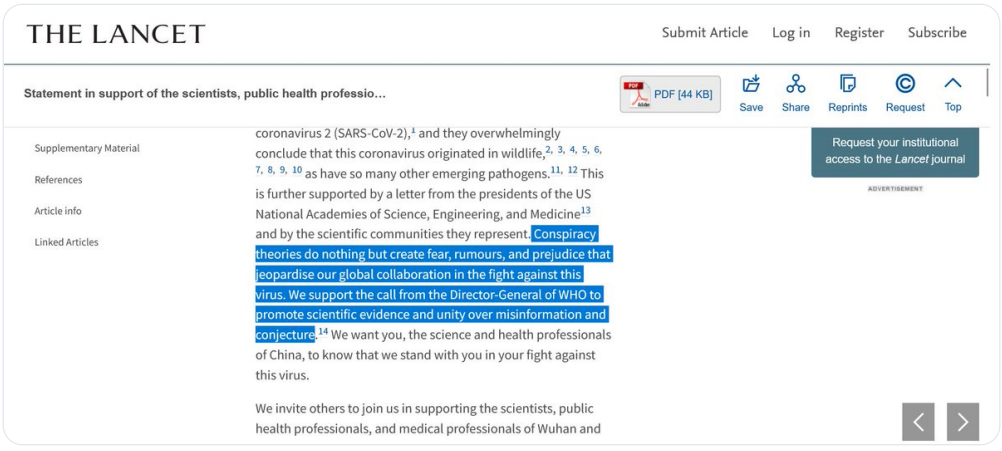
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We invite others to join us in supporting the scientists, public health professionals, and medical professionals of Wuhan and
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5🧵To me, Linda Saif is the red flag in the authors listed. A NAS Ohio State virologist who assisted the WHO during the 2003 SARS outbreak was a familiar name from FOIA'd emails between Baric, Daszak & Fauci from early on in 2020.

February 12, 2020

From: Su, Lishan <lishan_su@med.unc.edu>
Sent: Wednesday, February 12, 2020 1:12 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: A commentary on 2019 nCoV vs lab engineered viruses

Hi Ralph:

In response to the EMI journal editor's request, Drs. Shan-Lu Liu, Lin Saif and myself are writing a commentary (1-2 pages) to dispute the rumors of 2019 nCoV origin. Will you be interested, and have time, to have a quick read/comment? Please let me know if you have time.

Tentative Title: Is 2019-nCoV laboratory origin?

Thanks!

-Lishan

February 12, 2020

From: Saif, Linda
To: Liu, Shan-Lu; lishan_su@med.unc.edu
Subject: FW: A commentary on 2019 nCoV vs lab engineered viruses
Date: Wednesday, February 12, 2020 1:28:39 PM
Attachments: EMI-2019-nCoV_Commentary LJS_SLL_Refs-rsb.docx

Hi
Please note that Ralph made these changes on an earlier copy sent to him so hopefully the 2 of you can incorporate them into the updated draft I sent this AM!
Regards,
Linda

Linda J. Saif, PhD
Distinguished University Professor
Food Animal Health Research Program
OARDC/The Ohio State University
1680 Madison Ave
Wooster, Oh 44691

February 12, 2020

From: Su, Lishan <lishan_su@med.unc.edu>
Sent: Wednesday, February 12, 2020 10:11 AM
To: Baric, Ralph S <rbaric@email.unc.edu>
Subject: Re: A commentary on 2019 nCoV vs lab engineered viruses

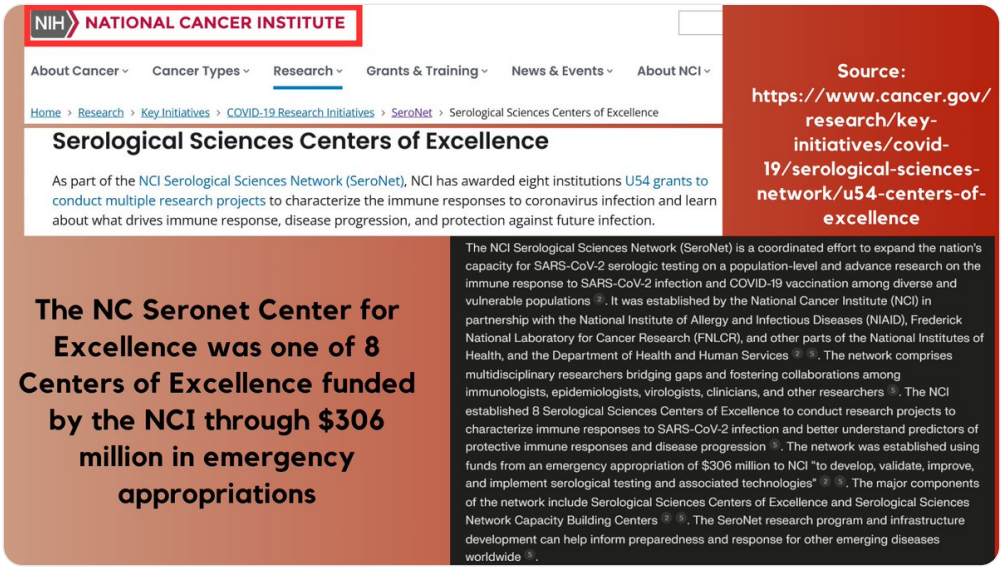
Hi Ralph:
We are trying to finish it and had no plan to get you too involved, but I do value your input. It is almost final and we are also getting comments from Perlman and Weiss.
Thanks,

-Lishan

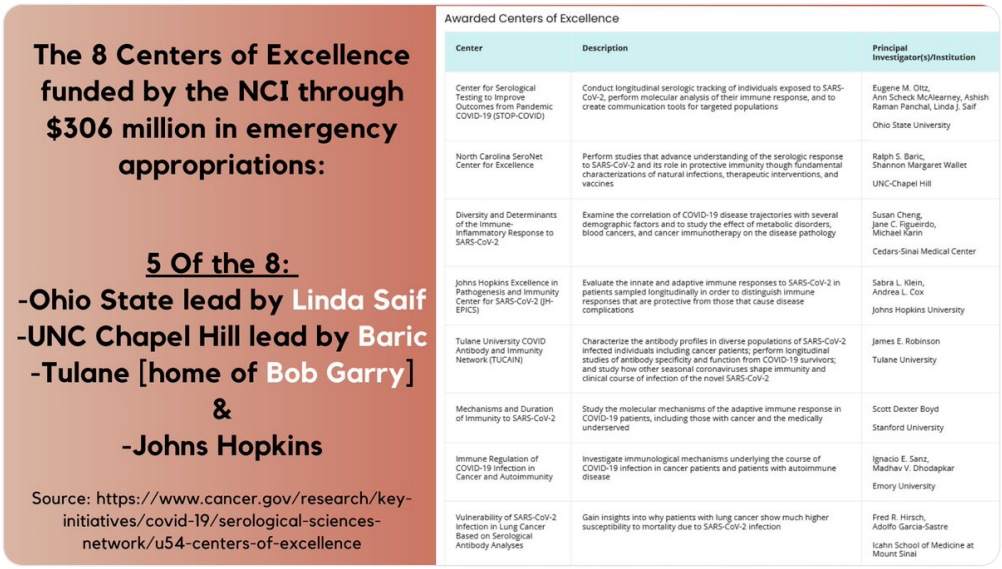
From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: Wednesday, February 12, 2020 at 10:02 AM
To: "Su, Lishan" <lishan_su@med.unc.edu>
Subject: RE: A commentary on 2019 nCoV vs lab engineered viruses

sure, but don't want to be cited in as having commented prior to submission.

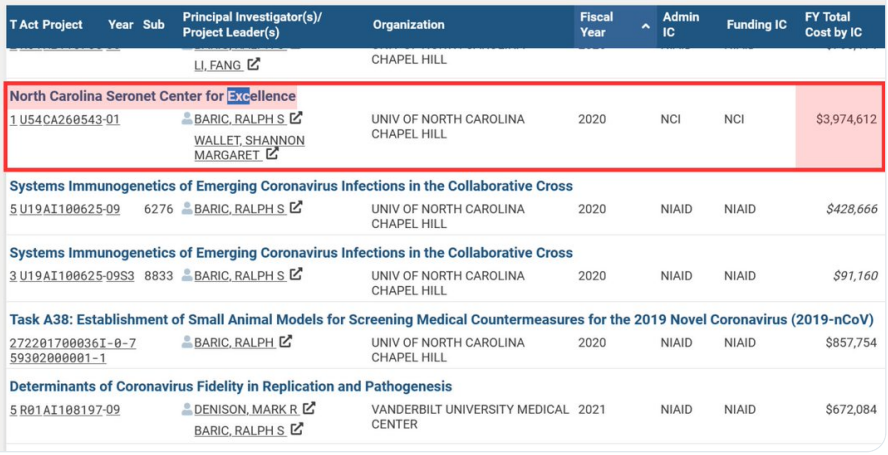
6🧵The emails show Saif and her co-workers emailing Baric about the paper in support of the Wuhan research. Why was she so concerned? I think I know why. While researching Baric's grants I found one for the NC Seronet Center for Excellence [NCSCE] Turns out the NCSCE is new!


NIH NATIONAL CANCER INSTITUTE
About Cancer
Cancer Types
Research
Grants & Training
News & Events
About NCI
Home › Research › Key Initiatives › COVID-19 Research Initiatives › SeroNet › Serological Sciences Centers of Excellence
Serological Sciences Centers of Excellence
As part of the NCI Serological Sciences Network (SeroNet), NCI has awarded eight institutions U54 grants to conduct multiple research projects to characterize the immune responses to coronavirus infection and learn about what drives immune response, disease progression, and protection against future infection.
Source: https://www.cancer.gov/research/key-initiatives/covid-19/serological-sciences-network/u54-centers-of-excellence
The NC Seronet Center for Excellence was one of 8 Centers of Excellence funded by the NCI through $306 million in emergency appropriations
The NCI Serological Sciences Network (SeroNet) is a coordinated effort to expand the nation's capacity for SARS-CoV-2 serologic testing on a population-level and advance research on the immune response to SARS-CoV-2 infection and COVID-19 vaccination among diverse and vulnerable populations. It was established by the National Cancer Institute (NCI) in partnership with the National Institute of Allergy and Infectious Diseases (NIAID), Frederick National Laboratory for Cancer Research (FNLCR), and other parts of the National Institutes of Health, and the Department of Health and Human Services. The network comprises multidisciplinary researchers bridging gaps and fostering collaborations among immunologists, epidemiologists, virologists, clinicians, and other researchers. The NCI established 8 Serological Sciences Centers of Excellence to conduct research projects to characterize immune responses to SARS-CoV-2 infection and better understand predictors of protective immune responses and disease progression. The network was established using funds from an emergency appropriation of $306 million to NCI "to develop, validate, improve, and implement serological testing and associated technologies". The major components of the network include Serological Sciences Centers of Excellence and Serological Sciences Network Capacity Building Centers. The SeroNet research program and infrastructure development can help inform preparedness and response for other emerging diseases worldwide.

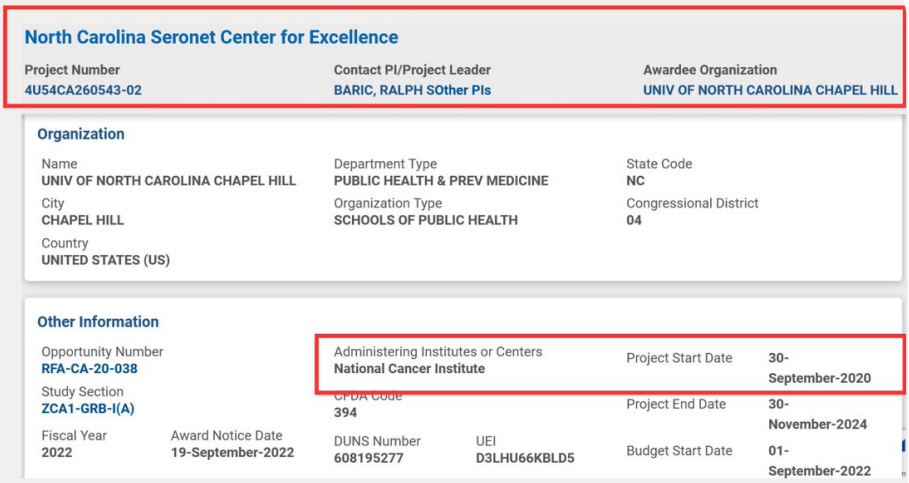
7🧵The NCSCE is one of 8 "Centers of Excellence" established w/a $306M fund- not by NIAID, but rather the National Cancer Institute even though the focus is on C19.🤔 Of the lucky 8 Centers created, Linda Saif of Ohio State was a recipient of a center just like Baric.💰😳


The 8 Centers of Excellence funded by the NCI through $306 million in emergency appropriations:
5 Of the 8:
-Ohio State lead by Linda Saif
-UNC Chapel Hill lead by Baric
-Tulane [home of Bob Garry]
&
-Johns Hopkins
Source: https://www.cancer.gov/research/key-initiatives/covid-19/serological-sciences-network/u54-centers-of-excellence
Awarded Centers of Excellence
Center | Description | Principal Investigator(s)/Institution
Center for Serological Testing to Improve Outcomes from Pandemic COVID-19 (STOP-COVID) | Conduct longitudinal serologic tracking of individuals exposed to SARS-CoV-2, perform molecular analysis of their immune response, and to create communication tools for targeted populations | Eugene M. Oltz, Ann Scheck McAlearney, Ashish Raman Panchal, Linda J. Saif, Ohio State University
North Carolina SeroNet Center for Excellence | Perform studies that advance understanding of the serologic response to SARS-CoV-2 and its role in protective immunity though fundamental characterizations of natural infections, therapeutic interventions, and vaccines | Ralph S. Baric, Shannon Margaret Wallet, UNC-Chapel Hill
Diversity and Determinants of the Immune-Inflammatory Response to SARS-CoV-2 | Examine the correlation of COVID-19 disease trajectories with several demographic factors and to study the effect of metabolic disorders, blood cancers, and cancer immunotherapy on the disease pathology | Susan Cheng, Jane C. Figueiredo, Michael Karin, Cedars-Sinai Medical Center
Johns Hopkins Excellence in Pathogenesis and Immunity Center for SARS-CoV-2 (JH-EPICS) | Evaluate the innate and adaptive immune responses to SARS-CoV-2 in patients sampled longitudinally in order to distinguish immune responses that are protective from those that cause disease complications | Sabra L. Klein, Andrea L. Cox, Johns Hopkins University
Tulane University COVID Antibody and Immunity Network (TUCAIN) | Characterize the antibody profiles in diverse populations of SARS-CoV-2 infected individuals including cancer patients; perform longitudinal studies of antibody specificity and function from COVID-19 survivors; and study how other seasonal coronaviruses shape immunity and clinical course of infection of the novel SARS-CoV-2 | James E. Robinson, Tulane University
Mechanisms and Duration of Immunity to SARS-CoV-2 | Study the molecular mechanisms of the adaptive immune response in COVID-19 patients, including those with cancer and the medically underserved | Scott Dexter Boyd, Stanford University
Immune Regulation of COVID-19 Infection in Cancer and Autoimmunity | Investigate immunological mechanisms underlying the course of COVID-19 infection in cancer patients and patients with autoimmune disease | Ignacio E. Sanz, Madhav V. Dhodapkar, Emory University
Vulnerability of SARS-CoV-2 Infection in Lung Cancer Based on Serological Antibody Analyses | Gain insights into why patients with lung cancer show much higher susceptibility to mortality due to SARS-CoV-2 infection | Fred R. Hirsch, Adolfo Garcia-Sastre, Icahn School of Medicine at Mount Sinai

Also in 2020, Baric receives a grant through the North Carolina Seronet Center for Excellence but its not funded by NIH/NIAID but rather by the National Cancer Institute for $3.9 Million dollars



T Act Project	Year	Sub	Principal Investigator(s)/ Project Leader(s)	Organization	Fiscal Year	Admin IC	Funding IC	FY Total Cost by IC
			LI, FANG	CHAPEL HILL				
North Carolina Seronet Center for Excellence								
1 U54CA260543-01			BARIC, RALPH S WALLET, SHANNON MARGARET	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NCI	NCI	$3,974,612
Systems Immunogenetics of Emerging Coronavirus Infections in the Collaborative Cross								
5 U19AI100625-09		6276	BARIC, RALPH S	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NIAID	NIAID	*$428,666*
Systems Immunogenetics of Emerging Coronavirus Infections in the Collaborative Cross								
3 U19AI100625-09S3		8833	BARIC, RALPH S	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NIAID	NIAID	*$91,160*
Task A38: Establishment of Small Animal Models for Screening Medical Countermeasures for the 2019 Novel Coronavirus (2019-nCoV)								
272201700036I-0-7 59302000001-1			BARIC, RALPH	UNIV OF NORTH CAROLINA CHAPEL HILL	2020	NIAID	NIAID	$857,754
Determinants of Coronavirus Fidelity in Replication and Pathogenesis								
5 R01AI108197-09			DENISON, MARK R BARIC, RALPH S	VANDERBILT UNIVERSITY MEDICAL CENTER	2021	NIAID	NIAID	$672,084



North Carolina Seronet Center for Excellence

Project Number	Contact PI/Project Leader	Awardee Organization
4U54CA260543-02	BARIC, RALPH SOther PIs	UNIV OF NORTH CAROLINA CHAPEL HILL

Organization

Name UNIV OF NORTH CAROLINA CHAPEL HILL	Department Type PUBLIC HEALTH & PREV MEDICINE	State Code NC
City CHAPEL HILL	Organization Type SCHOOLS OF PUBLIC HEALTH	Congressional District 04
Country UNITED STATES (US)		

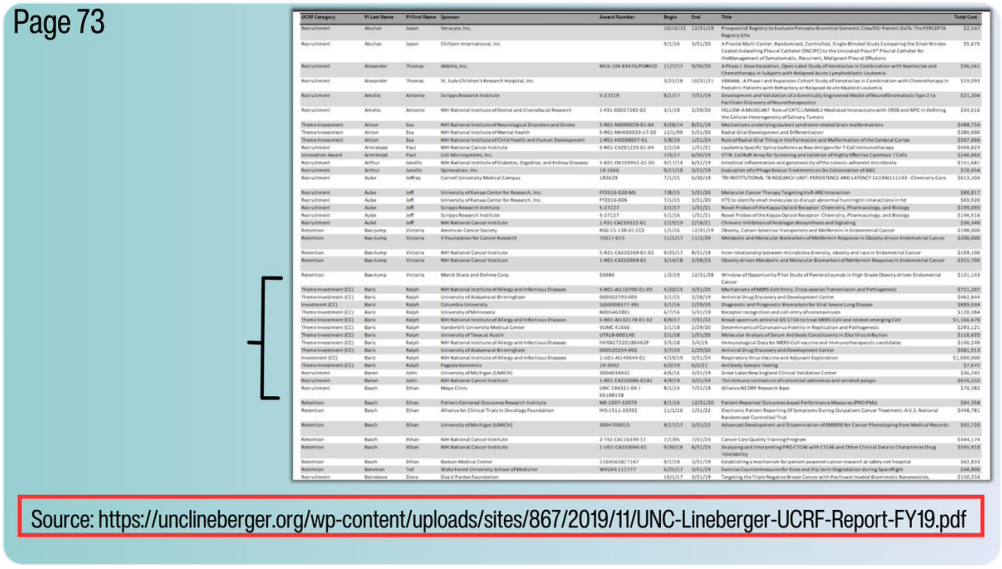
Other Information

Opportunity Number RFA-CA-20-038		Administering Institutes or Centers National Cancer Institute	Project Start Date	30-September-2020
Study Section ZCA1-GRB-I(A)		CFDA Code 394	Project End Date	30-November-2024
Fiscal Year 2022	Award Notice Date 19-September-2022	DUNS Number 608195277	UEI D3LHU66KBLD5	Budget Start Date 01-September-2022

8🧵Are you surprised by the funding being from NCI? I wasn't & only because I found that since 2019 more & more funds are going to Baric and not through NIH as much, but through the NCI. I have proof of this in UNC's Lineberger Cancer Institute's funding report for 2019...

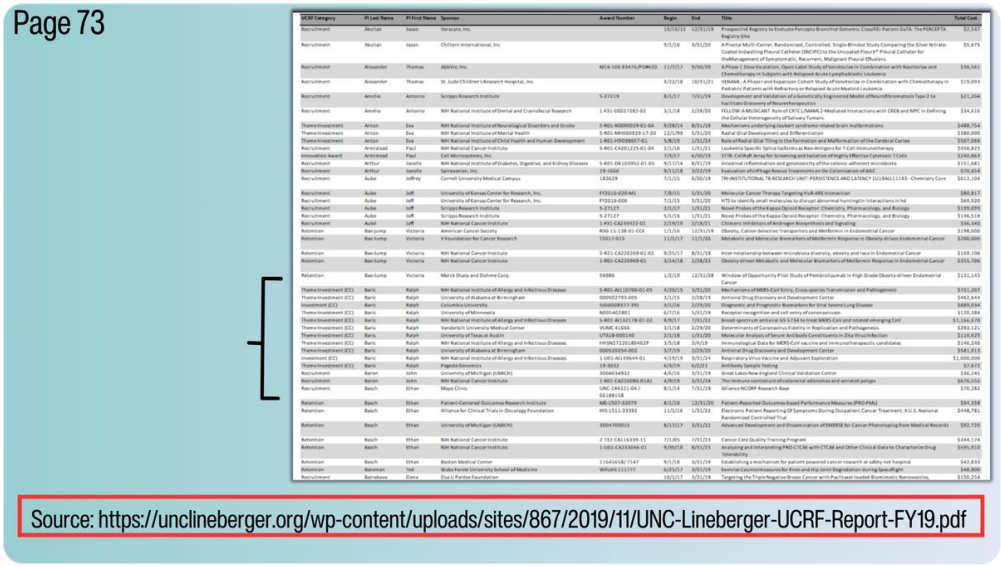
UNC LINEBERGER COMPREHENSIVE CANCER CENTER
UNIVERSITY CANCER RESEARCH FUND
2019 LEGISLATIVE REPORT
Annual Financial Report to the Joint Legislative Education Oversight Committee and the Office of State Budget and Management
Submitted November 1, 2019, in accordance with G.S.116-29.1
www.UNCLineberger.org/ucrf
INTRODUCTION
UNC LINEBERGER COMPREHENSIVE CANCER CENTER
UNIVERSITY CANCER RESEARCH FUND
2019 LEGISLATIVE REPORT
3
UNC LINEBERGER COMPREHENSIVE CANCER CENTER | UCRF 2019

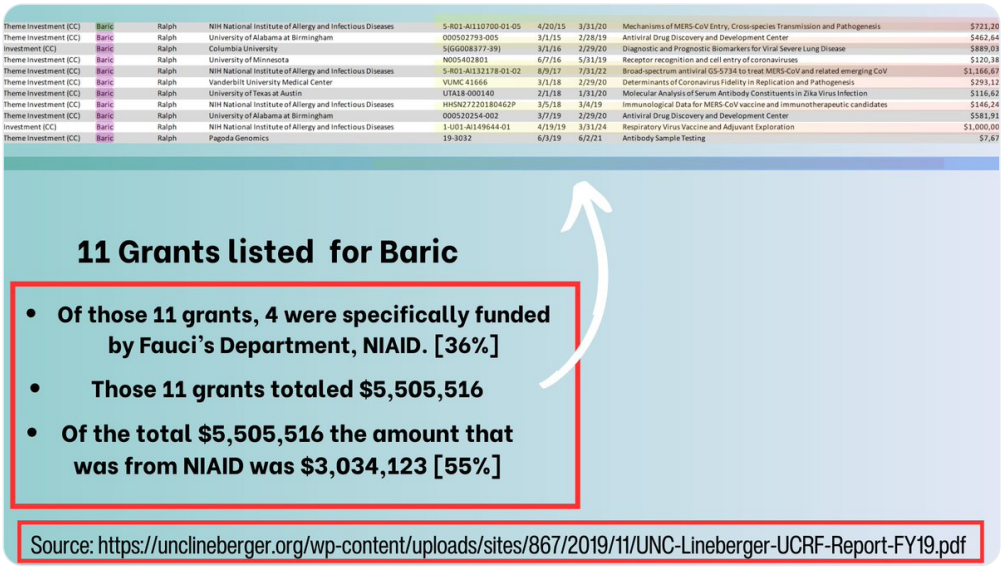
Source: https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf



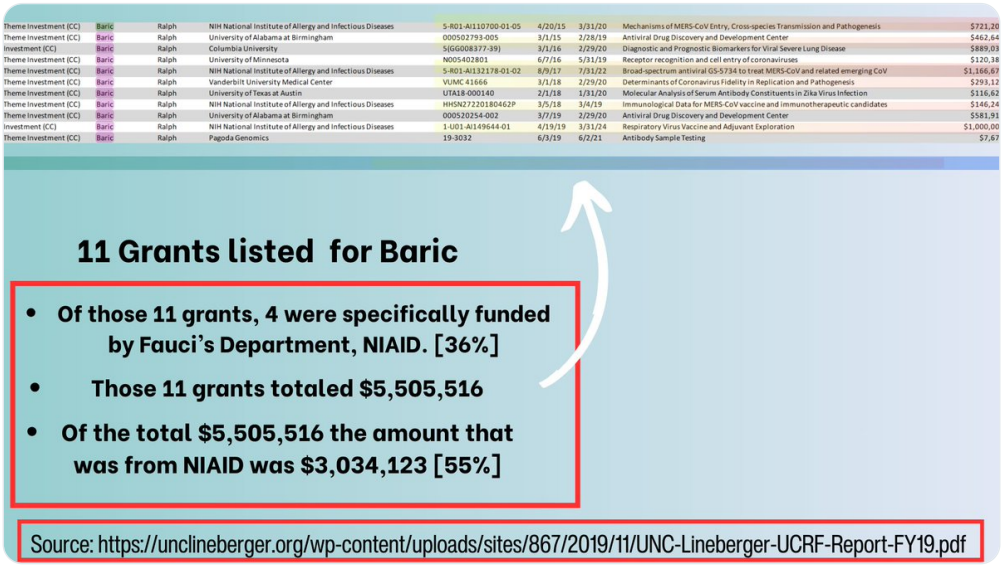
Source: https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf

9🧵On page 73, virologist [not oncologist] Ralph Baric is awarded 11 grants totaling over $5.5m! 55% of which came by way of the NIAID & 36% came from Fauci's NIAID. The two most financed grants, each over $1million say so much about how they put the "plan" in "plandemic."




Theme Investment (CC) Baric Ralph NIH National Institute of Allergy and Infectious Diseases 5-R01-AI110700-01-05 4/20/15 3/31/20 Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis $721,20
Theme Investment (CC) Baric Ralph University of Alabama at Birmingham 000502793-005 3/1/15 2/28/19 Antiviral Drug Discovery and Development Center $462,64
Investment (CC) Baric Ralph Columbia University 5(GG008377-39) 3/1/16 2/29/20 Diagnostic and Prognostic Biomarkers for Viral Severe Lung Disease $889,03
Theme Investment (CC) Baric Ralph University of Minnesota N005402801 6/7/16 5/31/19 Receptor recognition and cell entry of coronaviruses $120,38
Theme Investment (CC) Baric Ralph NIH National Institute of Allergy and Infectious Diseases 5-R01-AI132178-01-02 8/9/17 7/31/22 Broad-spectrum antiviral GS-5734 to treat MERS-CoV and related emerging CoV $1,166,67
Theme Investment (CC) Baric Ralph Vanderbilt University Medical Center VUMC 41666 3/1/18 2/29/20 Determinants of Coronavirus Fidelity in Replication and Pathogenesis $293,12
Theme Investment (CC) Baric Ralph University of Texas at Austin UTA18-000140 2/1/18 1/31/20 Molecular Analysis of Serum Antibody Constituents in Zika Virus Infection $116,62
Theme Investment (CC) Baric Ralph NIH National Institute of Allergy and Infectious Diseases HHSN272201804629 3/5/18 3/4/19 Immunological Data for MERS-CoV vaccine and immunotherapeutic candidates $146,24
Theme Investment (CC) Baric Ralph University of Alabama at Birmingham 000520254-002 3/7/19 2/29/20 Antiviral Drug Discovery and Development Center $581,91
Investment (CC) Baric Ralph NIH National Institute of Allergy and Infectious Diseases 1-U01-AI149644-01 4/19/19 3/31/24 Respiratory Virus Vaccine and Adjuvant Exploration $1,000,00
Theme Investment (CC) Baric Ralph Pagoda Genomics 19-3032 6/3/19 6/2/21 Antibody Sample Testing $7,67
11 Grants listed for Baric
• Of those 11 grants, 4 were specifically funded by Fauci's Department, NIAID. [36%]
• Those 11 grants totaled $5,505,516
• Of the total $5,505,516 the amount that was from NIAID was $3,034,123 [55%]
Source: https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf

10🧵One grant for Baric was for looking into GS-5743 to "treat emerging coronaviruses" & the other million dollar grant was for "Respiratory Virus Vaccine & Adjuvants" Mind you, this is a 2019 report & GS-5743, btw, is the C19/Ebola poison, Remdesivir.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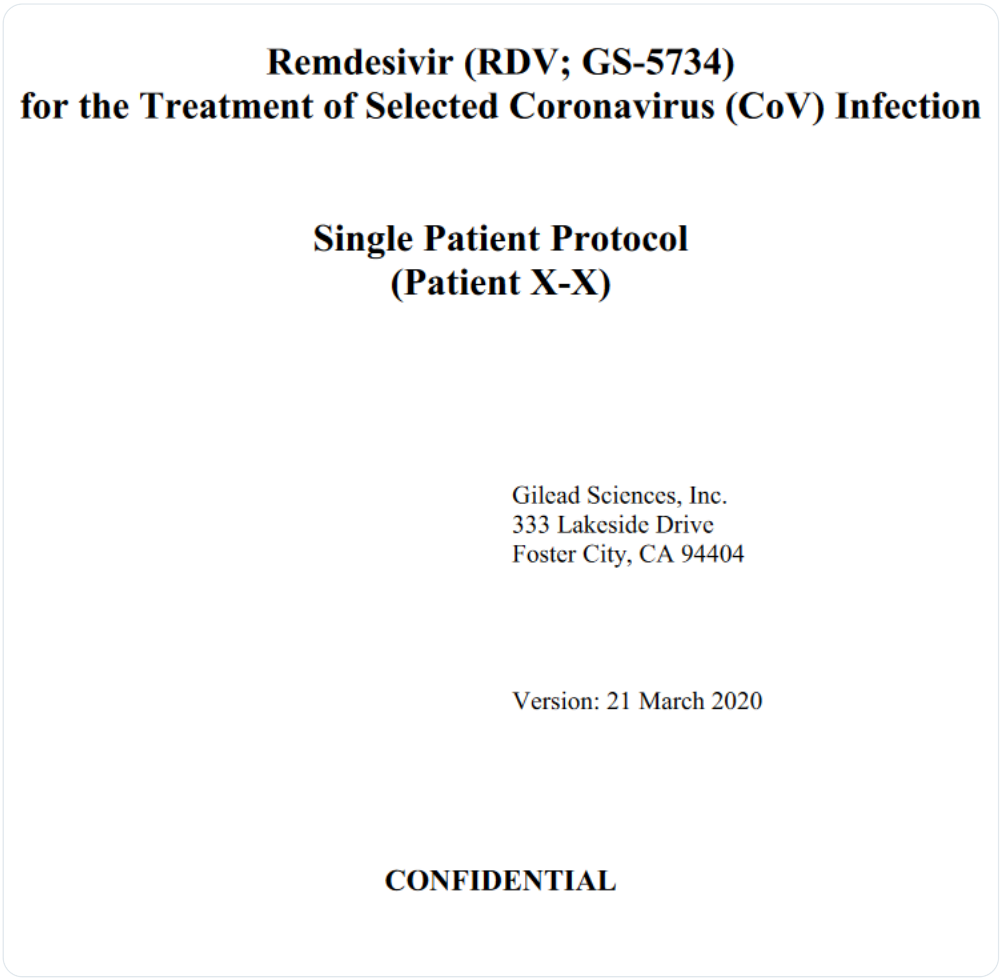
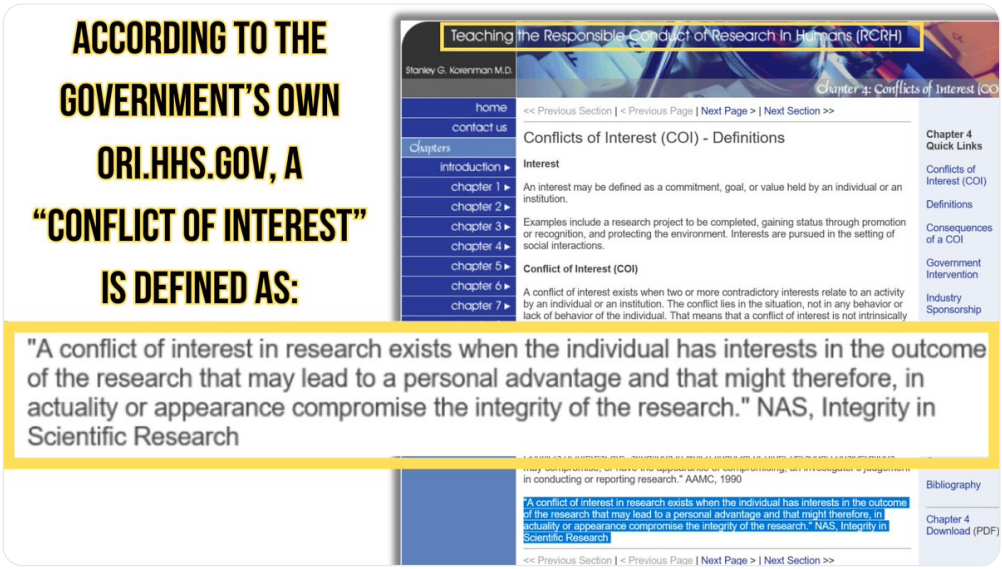


11🧵Lastly, I want to let the government & all implicated COVID criminals know that you guys are really good at playing the accidentally ignorant experts. You pretend your critics are conspiracy theorists but i know that YOU know the COIs/conspiracy plaguing you all. 👇U know!


ACCORDING TO THE GOVERNMENT'S OWN ORI.HHS.GOV, A "CONFLICT OF INTEREST" IS DEFINED AS:
Teaching the Responsible Conduct of Research in Humans (RCRH)
Stanley G. Korenman M.D.
Chapter 4: Conflicts of Interest (CO
home
contact us
Chapters
introduction
chapter 1
chapter 2
chapter 3
chapter 4
chapter 5
chapter 6
chapter 7
<< Previous Section | < Previous Page | Next Page > | Next Section >>
Conflicts of Interest (COI) - Definitions
Interest
An interest may be defined as a commitment, goal, or value held by an individual or an institution.
Examples include a research project to be completed, gaining status through promotion or recognition, and protecting the environment. Interests are pursued in the setting of social interactions.
Conflict of Interest (COI)
A conflict of interest exists when two or more contradictory interests relate to an activity by an individual or an institution. The conflict lies in the situation, not in any behavior or lack of behavior of the individual. That means that a conflict of interest is not intrinsically
Chapter 4 Quick Links
Conflicts of Interest (COI)
Definitions
Consequences of a COI
Government Intervention
Industry Sponsorship
"A conflict of interest in research exists when the individual has interests in the outcome of the research that may lead to a personal advantage and that might therefore, in actuality or appearance compromise the integrity of the research." NAS, Integrity in Scientific Research
in conducting or reporting research." AAMC, 1990
"A conflict of interest in research exists when the individual has interests in the outcome of the research that may lead to a personal advantage and that might therefore, in actuality or appearance compromise the integrity of the research." NAS, Integrity in Scientific Research
Bibliography
Chapter 4 Download (PDF)
<< Previous Section | < Previous Page | Next Page > | Next Section >>

12 🧾Receipts🔎

On behalf my friends, the vaccine injured: 🖕
You're gonna wish I took the jab, assholes. ✌️
I'm coming for the guilty. Bet on it. https://www.cancer.gov/research/key-initiatives/covid-19/serological-sciences-network/u54-centers-of-excellence
https://unclineberger.org/wp-content/uploads/sites/867/2019/11/UNC-Lineberger-UCRF-Report-FY19.pdf
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https://www.thelancet.com/action/showPdf?pii=S0140-6736%2820%2930418-9

Sources:

https://thenewamerican.com/world-news/china/wuhan-lab-workers-wife-died-after-covid-like-flu-in-december-2019/
https://s3.documentcloud.org/documents/6935295/NIH-Moderna-Confidential-Agreements.pdf
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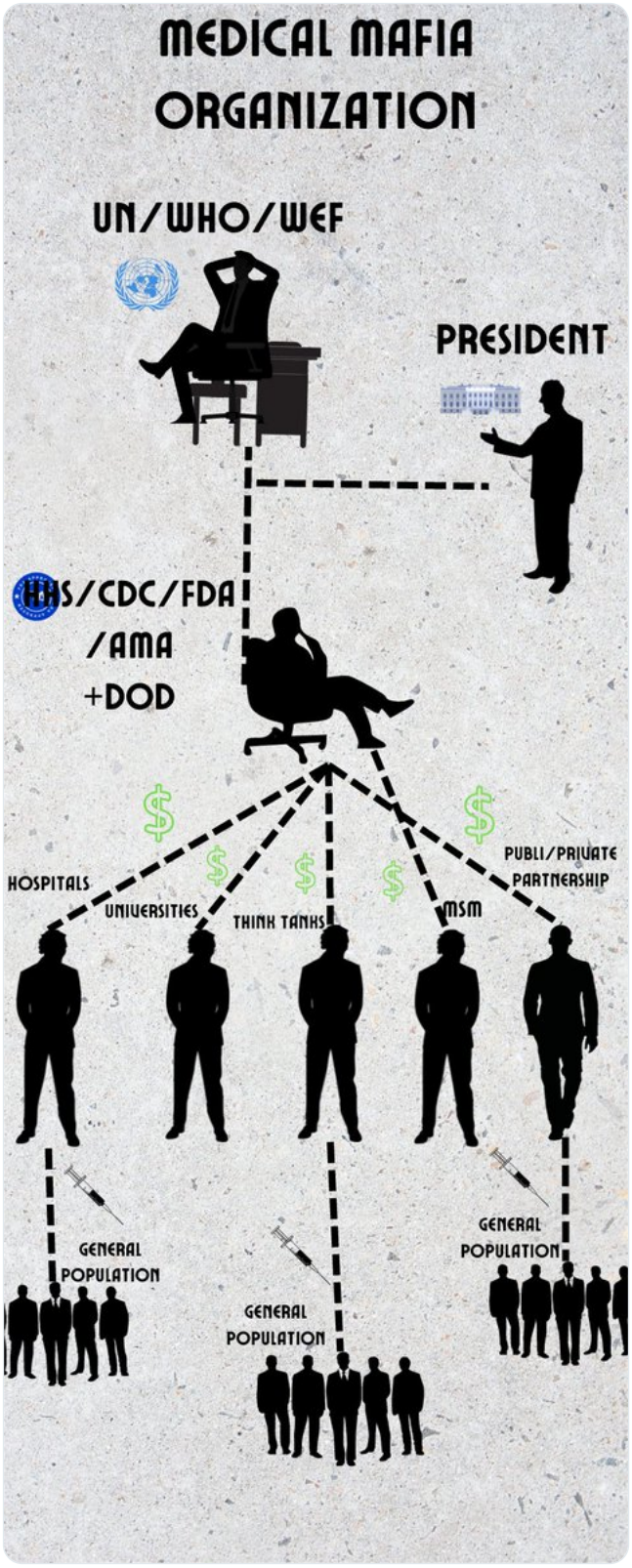
https://twitter.com/COVIDSelect/status/1730692429051826435



@threadreaderapp unroll

...

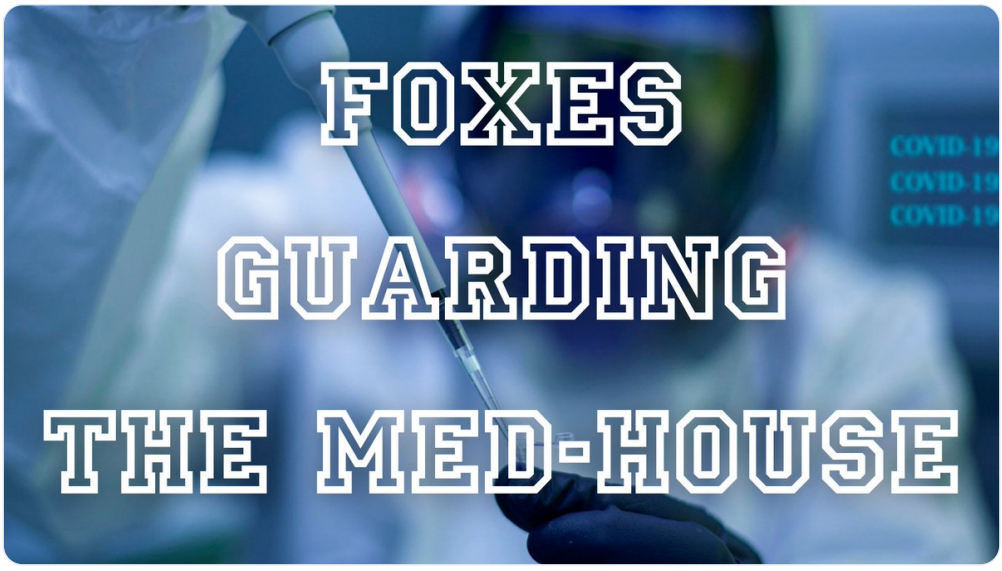
Destiny Rezendes @dezzie_rezzie

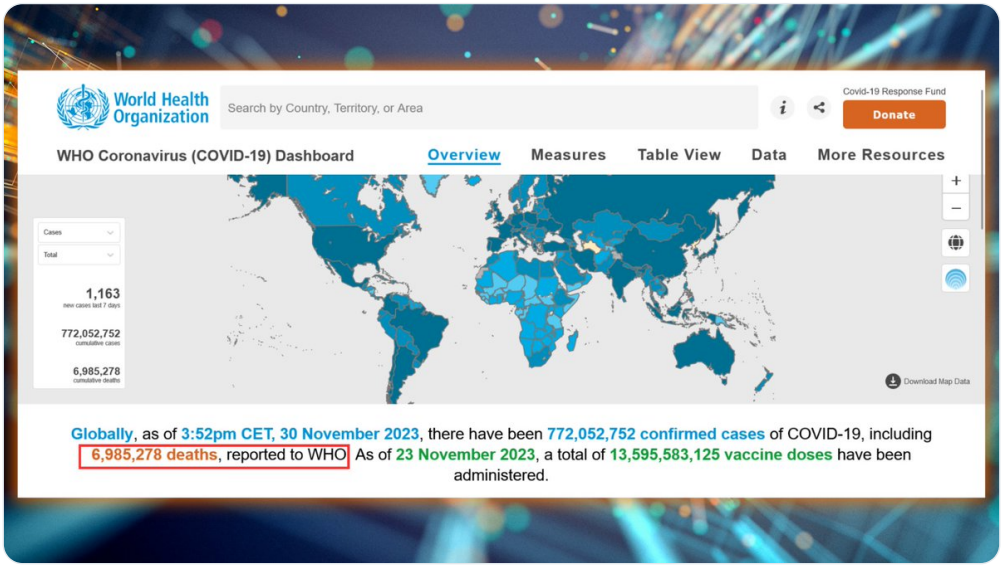
Dec 2, 2023 • 15 tweets • dezzie_rezzie/status/1731071621987782918

1🧵It's been 44months + 22 days since the birth of the C19 Pandemic-Claiming 5,125 deaths per day & yet funds haven't ended. No one has been jailed. No honest investigation has occurred. A death toll higher than what Hitler did to the Jews, but w/o a "Nuremberg 2.0" in sight.

6,985,278
DEATHS
https://www.cnn.com › 2022 › 03 › 07 › health › global-covid-deaths-surpass-six-million › in...
Global Covid-19 deaths surpass 6 million | CNN
Mar 7, 2022 · CNN — The global Covid-19 death toll surpassed 6 million on Monday, according to data from Johns Hopkins University. Global daily deaths have been dropping quickly over the past month,...

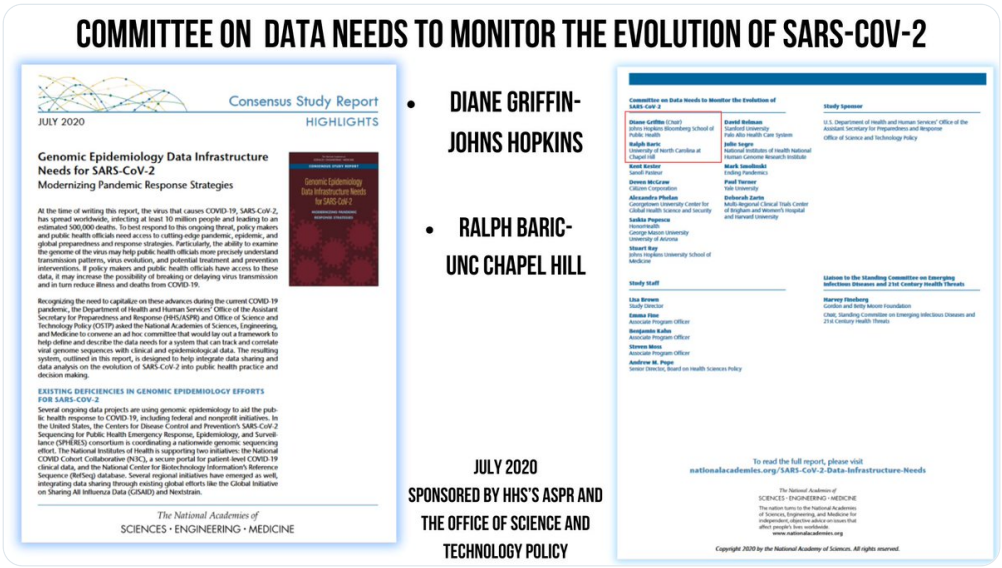
2🧵Over the course of the pandemic there has been a slew of oversight efforts that were tasked w/ investigating the origins of C19. In a just & honest world this would be reassuring but we don't live in that kind of world & the result is nothing short of abysmal.




World Health Organization
Search by Country, Territory, or Area
Covid-19 Response Fund
Donate
WHO Coronavirus (COVID-19) Dashboard
Overview
Measures
Table View
Data
More Resources
1,163
772,052,752
6,985,278
Globally, as of 3:52pm CET, 30 November 2023, there have been 772,052,752 confirmed cases of COVID-19, including 6,985,278 deaths, reported to WHO As of 23 November 2023, a total of 13,595,583,125 vaccine doses have been administered.

3🧵Let's take a look at a few of the oversight processes undertaken by our world & public health leaders. HHS's ASPR & the OSTP put/o a report on the early surveillance of C19: Committee on Data Needs to Monitor the Evolution of SARS-CoV-2, released July 2020.

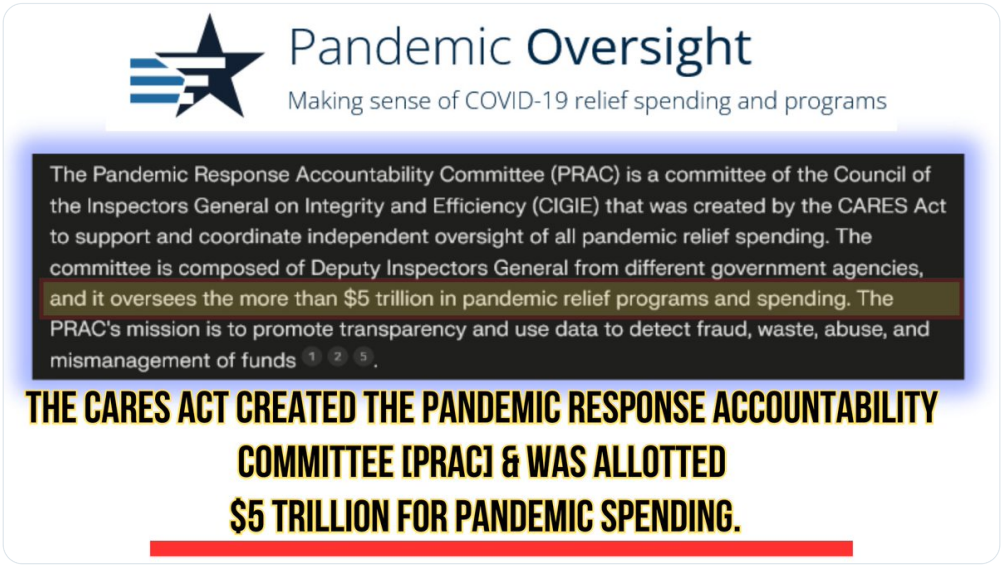
4🧵This committee was tasked w/ "track[ing] & correlate viral genome sequences" of early C19 genomic data. Listed first in the members roster is Diane Griffin of Johns Hopkins, followed immediately by GoF kingpin, Ralph Baricc of UNC Chapel HIll 👀


COMMITTEE ON DATA NEEDS TO MONITOR THE EVOLUTION OF SARS-COV-2
Consensus Study Report
JULY 2020
HIGHLIGHTS
Genomic Epidemiology Data Infrastructure Needs for SARS-CoV-2
Modernizing Pandemic Response Strategies
The National Academies of
SCIENCES · ENGINEERING · MEDICINE
DIANE GRIFFIN- JOHNS HOPKINS
RALPH BARIC- UNC CHAPEL HILL
JULY 2020
SPONSORED BY HHS'S ASPR AND THE OFFICE OF SCIENCE AND TECHNOLOGY POLICY

5🧵Next, the Pandemic Response Accountability Committee [PRAC]. PRAC, also called "Pandemic Oversight" was established with the enactment of the CARES Act. The committee is composed of Inspector Generals and they oversee a historic 5 TRILLION dollars of pandemic relief funds.

Pandemic Oversight
Making sense of COVID-19 relief spending and programs
The Pandemic Response Accountability Committee (PRAC) is a committee of the Council of the Inspectors General on Integrity and Efficiency (CIGIE) that was created by the CARES Act to support and coordinate independent oversight of all pandemic relief spending. The committee is composed of Deputy Inspectors General from different government agencies, and it oversees the more than $5 trillion in pandemic relief programs and spending. The PRAC's mission is to promote transparency and use data to detect fraud, waste, abuse, and mismanagement of funds 1 2 5.
THE CARES ACT CREATED THE PANDEMIC RESPONSE ACCOUNTABILITY COMMITTEE [PRAC] & WAS ALLOTTED $5 TRILLION FOR PANDEMIC SPENDING.

6🧵The PRAC's 5 TRILLION dollar fund base is insane. $5 trillion is roughly 15% of our debt [33.8t] This makes the $5-10bn Project Bioshield Act of 2004 look like pennies. Who's on the board? Health experts? There's ONE, but don't worry the Federal Reserve & NASA are on it! 🤦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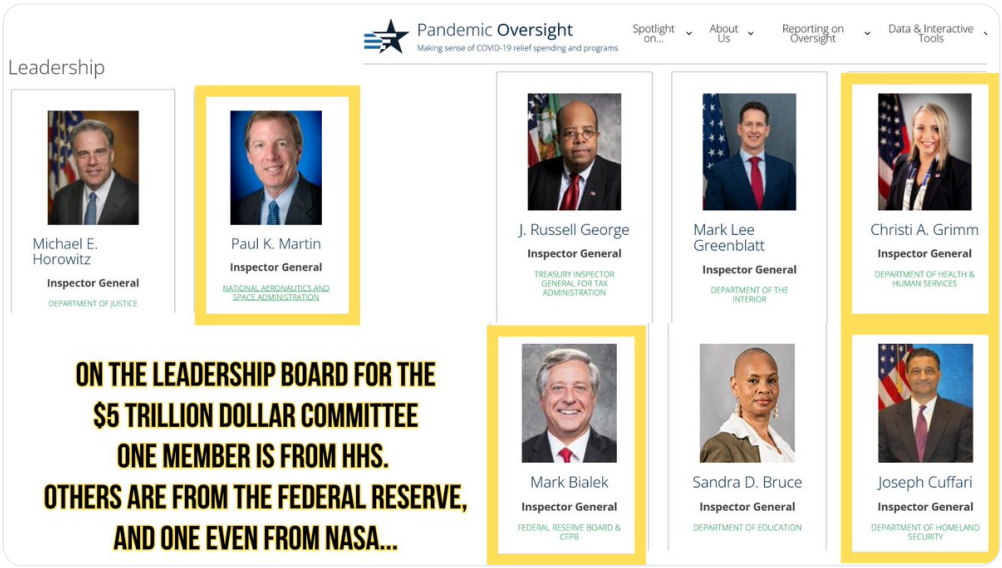
THE CARES ACT CREATED THE PANDEMIC RESPONSE ACCOUNTABILITY COMMITTEE [PRAC] & WAS ALLOTTED $5 TRILLION FOR PANDEMIC SPENDING.



7🧵The WHO convened a Global Study into the origins of SARS COV2. This was supposed to be the most official & conclusive report second only to the intelligence report. Presenters included Koopmans, the Bat Lady, & Peter Daszak of EcoHealth Alliance

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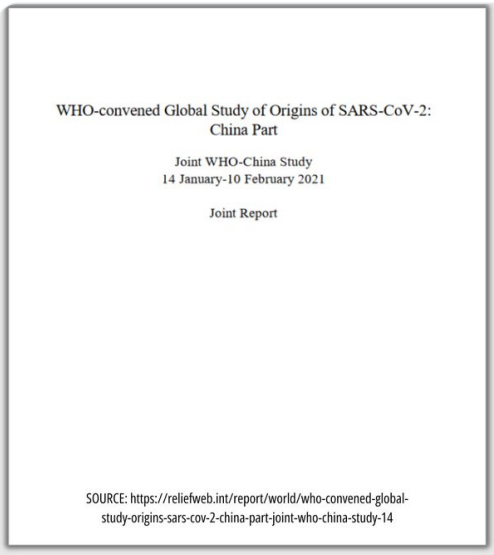
WHO-convened Global Study of Origins of SARS-CoV-2: China Part | Joint WHO-China Study, 14 January-10 February 2021
Analysis • Source: WHO • Posted: 30 Mar 2021 • Originally published: 30 Mar 2021 • Origin: View original
Background information
From the very beginning of the pandemic WHO has stressed the need to understand the origin of the virus in order to better understand the emergence of new pathogens and possible exposures.
Primary country:
World
Other country:
China

SOURCE: HTTPS://RELIEFWEB.INT/REPORT/WORLD/WHO-CONVENED-GLOBAL-STUDY-ORIGINS-SARS-COV-2-CHINA-PART-JOINT-WHO-CHINA-STUDY-14

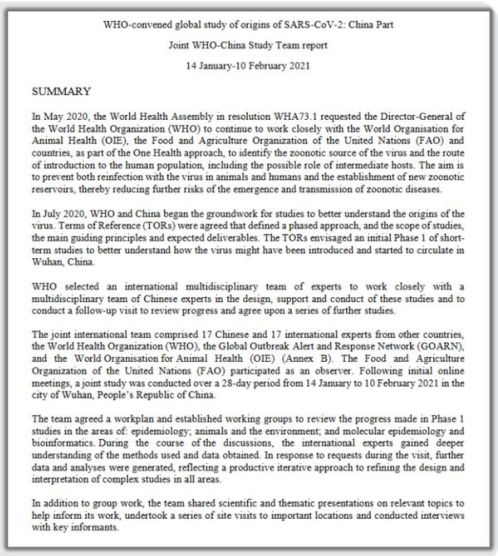


WHO-convened Global Study of Origins of SARS-CoV-2: China Part

Joint WHO-China Study
14 January-10 February 2021

Joint Report

SOURCE: https://reliefweb.int/report/world/who-convened-global-study-origins-sars-cov-2-china-part-joint-who-china-study-14



WHO-convened global study of origins of SARS-CoV-2: China Part

Joint WHO-China Study Team report

14 January-10 February 2021

SUMMARY

In May 2020, the World Health Assembly in resolution WHA73.1 requested the Director-General of the World Health Organization (WHO) to continue to work closely with the World Organisation for Animal Health (OIE), the Food and Agriculture Organization of the United Nations (FAO) and countries, as part of the One Health approach, to identify the zoonotic source of the virus and the route of introduction to the human population, including the possible role of intermediate hosts. The aim is to prevent both reinfection with the virus in animals and humans and the establishment of new zoonotic reservoirs, thereby reducing further risks of the emergence and transmission of zoonotic diseases.

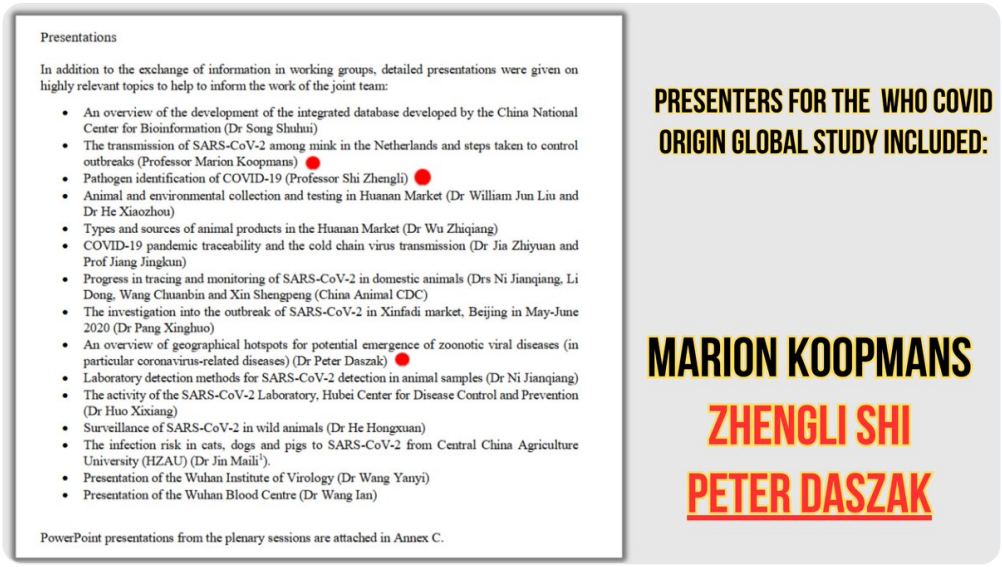
In July 2020, WHO and China began the groundwork for studies to better understand the origins of the virus. Terms of Reference (TORs) were agreed that defined a phased approach, and the scope of studies, the main guiding principles and expected deliverables. The TORs envisaged an initial Phase 1 of short-term studies to better understand how the virus might have been introduced and started to circulate in Wuhan, China.

WHO selected an international multidisciplinary team of experts to work closely with a multidisciplinary team of Chinese experts in the design, support and conduct of these studies and to conduct a follow-up visit to review progress and agree upon a series of further studies.

The joint international team comprised 17 Chinese and 17 international experts from other countries, the World Health Organization (WHO), the Global Outbreak Alert and Response Network (GOARN), and the World Organisation for Animal Health (OIE) (Annex B). The Food and Agriculture Organization of the United Nations (FAO) participated as an observer. Following initial online meetings, a joint study was conducted over a 28-day period from 14 January to 10 February 2021 in the city of Wuhan, People's Republic of China.

The team agreed a workplan and established working groups to review the progress made in Phase 1 studies in the areas of: epidemiology; animals and the environment; and molecular epidemiology and bioinformatics. During the course of the discussions, the international experts gained deeper understanding of the methods used and data obtained. In response to requests during the visit, further data and analyses were generated, reflecting a productive iterative approach to refining the design and interpretation of complex studies in all areas.

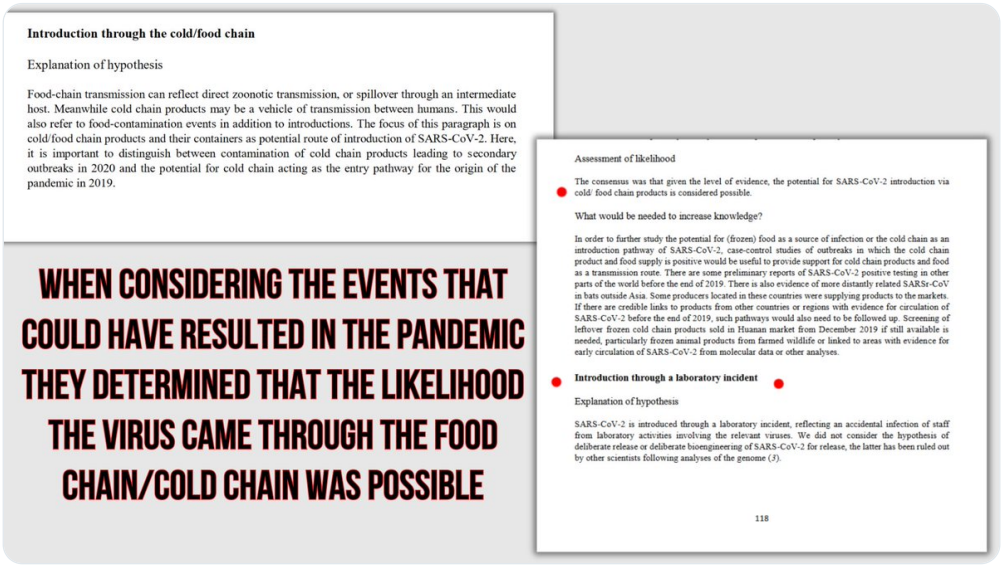
In addition to group work, the team shared scientific and thematic presentations on relevant topics to help inform its work, undertook a series of site visits to important locations and conducted interviews with key informants.

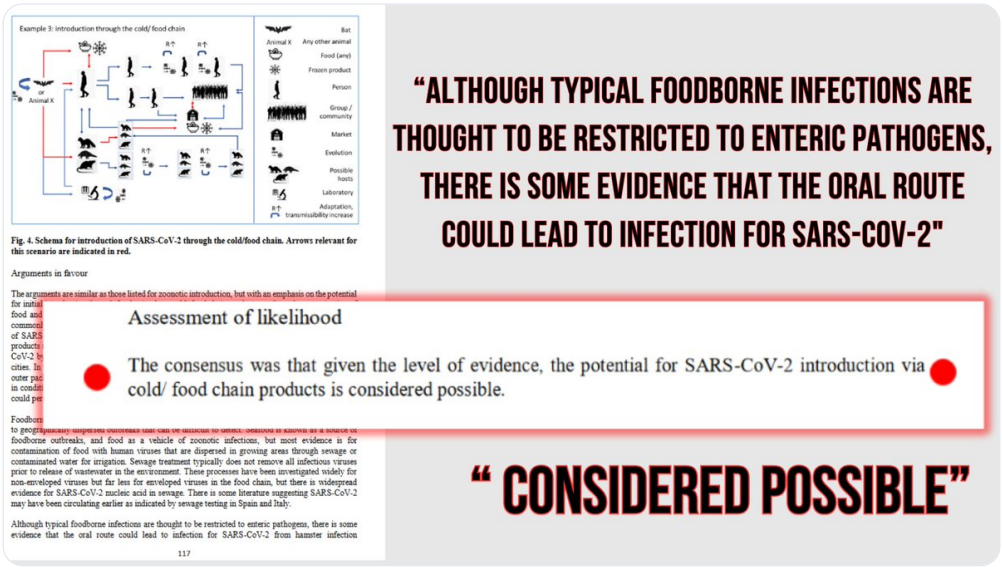

Presentations
In addition to the exchange of information in working groups, detailed presentations were given on highly relevant topics to help to inform the work of the joint team:
An overview of the development of the integrated database developed by the China National Center for Bioinformation (Dr Song Shuhui)
The transmission of SARS-CoV-2 among mink in the Netherlands and steps taken to control outbreaks (Professor Marion Koopmans)
Pathogen identification of COVID-19 (Professor Shi Zhengli)
Animal and environmental collection and testing in Huanan Market (Dr William Jun Liu and Dr He Xiaozhou)
Types and sources of animal products in the Huanan Market (Dr Wu Zhiqiang)
COVID-19 pandemic traceability and the cold chain virus transmission (Dr Jia Zhiyuan and Prof Jiang Jingkun)
Progress in tracing and monitoring of SARS-CoV-2 in domestic animals (Drs Ni Jianqiang, Li Dong, Wang Chuanbin and Xin Shengpeng (China Animal CDC)
The investigation into the outbreak of SARS-CoV-2 in Xinfadi market, Beijing in May-June 2020 (Dr Pang Xinghuo)
An overview of geographical hotspots for potential emergence of zoonotic viral diseases (in particular coronavirus-related diseases) (Dr Peter Daszak)
Laboratory detection methods for SARS-CoV-2 detection in animal samples (Dr Ni Jianqiang)
The activity of the SARS-CoV-2 Laboratory, Hubei Center for Disease Control and Prevention (Dr Huo Xixiang)
Surveillance of SARS-CoV-2 in wild animals (Dr He Hongxuan)
The infection risk in cats, dogs and pigs to SARS-CoV-2 from Central China Agriculture University (HZAU) (Dr Jin Maili[1]).
Presentation of the Wuhan Institute of Virology (Dr Wang Yanyi)
Presentation of the Wuhan Blood Centre (Dr Wang Ian)
PowerPoint presentations from the plenary sessions are attached in Annex C.
PRESENTERS FOR THE WHO COVID ORIGIN GLOBAL STUDY INCLUDED:
MARION KOOPMANS
ZHENGLI SHI
PETER DASZAK

8🧵The last 50pgs lay out the possible ways the pandemic could have started. They examined zoonotic spillover, food chain contamination, intermediate hosts, & a lab leak.

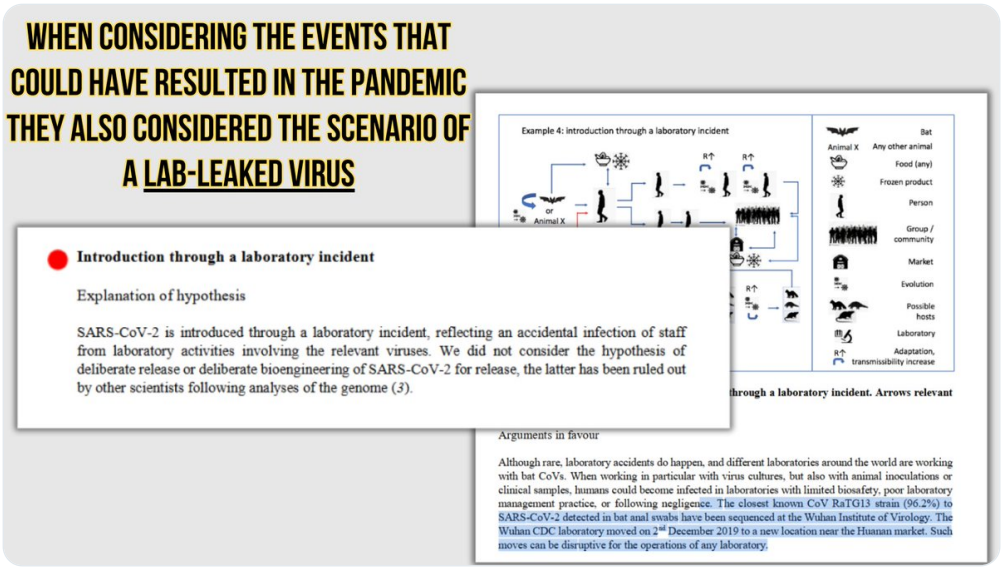
Joint Report
WHO-convened Global Study of Origins of SARS-CoV-2: China Part | J…
Analysis in English on World and 1 other country about Health and Epidemic; published on 30 Mar 2021 by WHO
https://reliefweb.int/report/world/who-convened-global-study-origins-sars-cov-2-china-p…

9🧵The idea that C19 came from contamination w/in the food/cold chain w/ infected zoonotic interactions sounded ridiculous to me, but the WHO thought that this scenario had merit & they deemed it "considered possible" 🤣

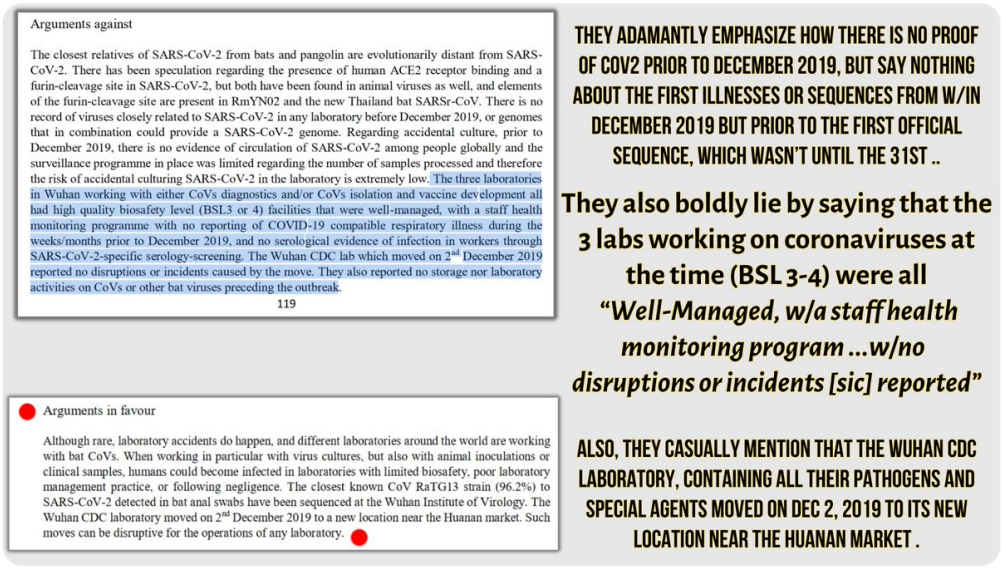

Introduction through the cold/food chain
Explanation of hypothesis
Food-chain transmission can reflect direct zoonotic transmission, or spillover through an intermediate host. Meanwhile cold chain products may be a vehicle of transmission between humans. This would also refer to food-contamination events in addition to introductions. The focus of this paragraph is on cold/food chain products and their containers as potential route of introduction of SARS-CoV-2. Here, it is important to distinguish between contamination of cold chain products leading to secondary outbreaks in 2020 and the potential for cold chain acting as the entry pathway for the origin of the pandemic in 2019.
WHEN CONSIDERING THE EVENTS THAT COULD HAVE RESULTED IN THE PANDEMIC THEY DETERMINED THAT THE LIKELIHOOD THE VIRUS CAME THROUGH THE FOOD CHAIN/COLD CHAIN WAS POSSIBLE
Assessment of likelihood
The consensus was that given the level of evidence, the potential for SARS-CoV-2 introduction via cold/ food chain products is considered possible.
What would be needed to increase knowledge?
In order to further study the potential for (frozen) food as a source of infection or the cold chain as an introduction pathway of SARS-CoV-2, case-control studies of outbreaks in which the cold chain product and food supply is positive would be useful to provide support for cold chain products and food as a transmission route. There are some preliminary reports of SARS-CoV-2 positive testing in other parts of the world before the end of 2019. There is also evidence of more distantly related SARSr-CoV in bats outside Asia. Some producers located in these countries were supplying products to the markets. If there are credible links to products from other countries or regions with evidence for circulation of SARS-CoV-2 before the end of 2019, such pathways would also need to be followed up. Screening of leftover frozen cold chain products sold in Huanan market from December 2019 if still available is needed, particularly frozen animal products from farmed wildlife or linked to areas with evidence for early circulation of SARS-CoV-2 from molecular data or other analyses.
Introduction through a laboratory incident
Explanation of hypothesis
SARS-CoV-2 is introduced through a laboratory incident, reflecting an accidental infection of staff from laboratory activities involving the relevant viruses. We did not consider the hypothesis of deliberate release or deliberate bioengineering of SARS-CoV-2 for release, the latter has been ruled out by other scientists following analyses of the genome (3).
118


Example 3: introduction through the cold/ food chain
Bat
Animal X
Any other animal
Food (any)
Frozen product
Person
Group / community
Market
Evolution
Possible hosts
Laboratory
Adaptation, transmissibility increase
Fig. 4. Schema for introduction of SARS-CoV-2 through the cold/food chain. Arrows relevant for this scenario are indicated in red.
Arguments in favour
foodborne outbreaks, and food as a vehicle of zoonotic infections, but most evidence is for contamination of food with human viruses that are dispersed in growing areas through sewage or contaminated water for irrigation. Sewage treatment typically does not remove all infectious viruses prior to release of wastewater in the environment. These processes have been investigated widely for non-enveloped viruses but far less for enveloped viruses in the food chain, but there is widespread evidence for SARS-CoV-2 nucleic acid in sewage. There is some literature suggesting SARS-CoV-2 may have been circulating earlier as indicated by sewage testing in Spain and Italy.
Although typical foodborne infections are thought to be restricted to enteric pathogens, there is some evidence that the oral route could lead to infection for SARS-CoV-2 from hamster infection
117
"ALTHOUGH TYPICAL FOODBORNE INFECTIONS ARE THOUGHT TO BE RESTRICTED TO ENTERIC PATHOGENS, THERE IS SOME EVIDENCE THAT THE ORAL ROUTE COULD LEAD TO INFECTION FOR SARS-COV-2"
Assessment of likelihood
The consensus was that given the level of evidence, the potential for SARS-CoV-2 introduction via cold/ food chain products is considered possible.
" CONSIDERED POSSIBLE"

10🧵The lab-leak hypothesis was the last one they covered & compared to other theories was only lightly discussed & all credible circumstantial evidence was downplayed. They completely ignore the possibility that it may have been released in 2019 & furthermore...

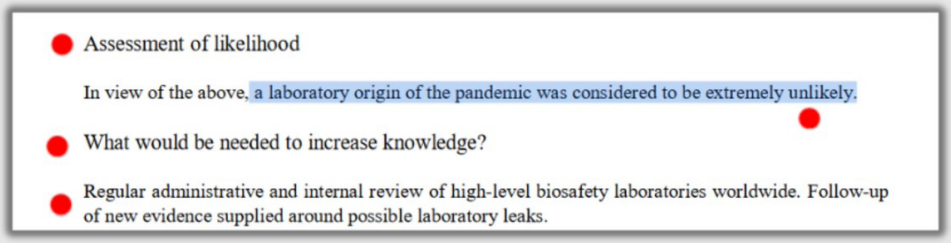

WHEN CONSIDERING THE EVENTS THAT COULD HAVE RESULTED IN THE PANDEMIC THEY ALSO CONSIDERED THE SCENARIO OF A LAB-LEAKED VIRUS
Example 4: introduction through a laboratory incident
Bat
Animal X
Any other animal
Food (any)
Frozen product
Person
Group / community
Market
Evolution
Possible hosts
Laboratory
Adaptation, transmissibility increase
Introduction through a laboratory incident
Explanation of hypothesis
SARS-CoV-2 is introduced through a laboratory incident, reflecting an accidental infection of staff from laboratory activities involving the relevant viruses. We did not consider the hypothesis of deliberate release or deliberate bioengineering of SARS-CoV-2 for release, the latter has been ruled out by other scientists following analyses of the genome (3).
through a laboratory incident. Arrows relevant
Arguments in favour
Although rare, laboratory accidents do happen, and different laboratories around the world are working with bat CoVs. When working in particular with virus cultures, but also with animal inoculations or clinical samples, humans could become infected in laboratories with limited biosafety, poor laboratory management practice, or following negligence. The closest known CoV RaTG13 strain (96.2%) to SARS-CoV-2 detected in bat anal swabs have been sequenced at the Wuhan Institute of Virology. The Wuhan CDC laboratory moved on 2nd December 2019 to a new location near the Huanan market. Such moves can be disruptive for the operations of any laboratory.

11🧵They report blatant lies-claiming all the labs doing CoV research in BSL3-4 labs were all up to standard, well maintained & had no record of lab incidents. [Pandora's Gamble proves this to be a lie.] & WIVs CDC lab relocation had no bearing on the safety..


Arguments against
The closest relatives of SARS-CoV-2 from bats and pangolin are evolutionarily distant from SARS-CoV-2. There has been speculation regarding the presence of human ACE2 receptor binding and a furin-cleavage site in SARS-CoV-2, but both have been found in animal viruses as well, and elements of the furin-cleavage site are present in RmYN02 and the new Thailand bat SARSr-CoV. There is no record of viruses closely related to SARS-CoV-2 in any laboratory before December 2019, or genomes that in combination could provide a SARS-CoV-2 genome. Regarding accidental culture, prior to December 2019, there is no evidence of circulation of SARS-CoV-2 among people globally and the surveillance programme in place was limited regarding the number of samples processed and therefore the risk of accidental culturing SARS-CoV-2 in the laboratory is extremely low. The three laboratories in Wuhan working with either CoVs diagnostics and/or CoVs isolation and vaccine development all had high quality biosafety level (BSL3 or 4) facilities that were well-managed, with a staff health monitoring programme with no reporting of COVID-19 compatible respiratory illness during the weeks/months prior to December 2019, and no serological evidence of infection in workers through SARS-CoV-2-specific serology-screening. The Wuhan CDC lab which moved on 2nd December 2019 reported no disruptions or incidents caused by the move. They also reported no storage nor laboratory activities on CoVs or other bat viruses preceding the outbreak.
119
Arguments in favour
Although rare, laboratory accidents do happen, and different laboratories around the world are working with bat CoVs. When working in particular with virus cultures, but also with animal inoculations or clinical samples, humans could become infected in laboratories with limited biosafety, poor laboratory management practice, or following negligence. The closest known CoV RaTG13 strain (96.2%) to SARS-CoV-2 detected in bat anal swabs have been sequenced at the Wuhan Institute of Virology. The Wuhan CDC laboratory moved on 2nd December 2019 to a new location near the Huanan market. Such moves can be disruptive for the operations of any laboratory.
THEY ADAMANTLY EMPHASIZE HOW THERE IS NO PROOF OF COV2 PRIOR TO DECEMBER 2019, BUT SAY NOTHING ABOUT THE FIRST ILLNESSES OR SEQUENCES FROM W/IN DECEMBER 2019 BUT PRIOR TO THE FIRST OFFICIAL SEQUENCE, WHICH WASN'T UNTIL THE 31ST ..
They also boldly lie by saying that the 3 labs working on coronaviruses at the time (BSL 3-4) were all "Well-Managed, w/a staff health monitoring program ...w/no disruptions or incidents [sic] reported"
ALSO, THEY CASUALLY MENTION THAT THE WUHAN CDC LABORATORY, CONTAINING ALL THEIR PATHOGENS AND SPECIAL AGENTS MOVED ON DEC 2, 2019 TO ITS NEW LOCATION NEAR THE HUANAN MARKET .

12🧵The report's consensus was a lab leak was "considered extremely unlikely." 😑 And what indisputable evidence did they cite for this conclusion? An EcoHealth Alliance paper & the fraudulently infamous "Proximal Origins" paper! Solid investigating, WHO! Good job. 🤦‍♀️SMH

THEIR CONCLUSION ON WHETHER OR NOT A LAB LEAK WAS RESPONSIBLE FOR COVID-19?



Assessment of likelihood

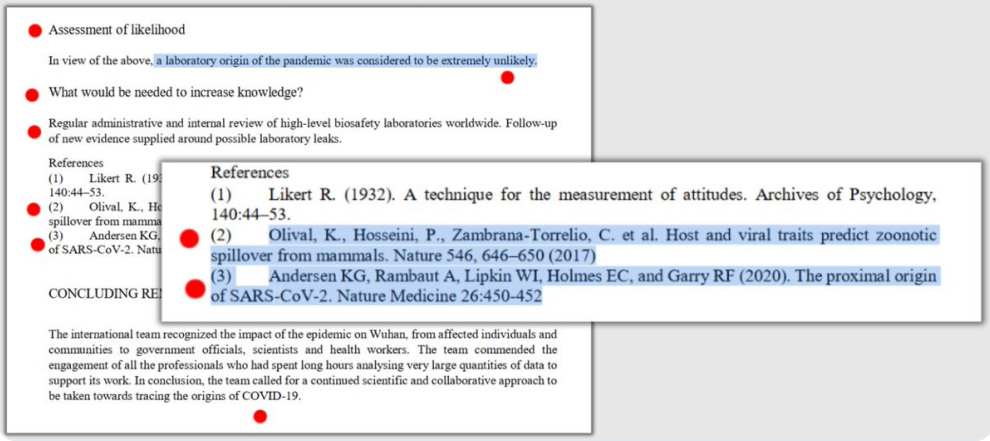
In view of the above, a laboratory origin of the pandemic was considered to be extremely unlikely.

What would be needed to increase knowledge?

Regular administrative and internal review of high-level biosafety laboratories worldwide. Follow-up of new evidence supplied around possible laboratory leaks.

"A Laboratory origin of the pandemic was considered to be extremely unlikely."

To top it all off the references listed for this claim that a lab leak was unlikely [of the 3 citations] one is an EcoHealth Alliance Paper, and the other is the infamously fraudulent "Proximal Origins" paper.



Assessment of likelihood

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References

(1) Likert R. (19
140:44–53.
(2) Olival, K., Ho
spillover from mamma
(3) Andersen KG,
of SARS-CoV-2. Natu

CONCLUDING RE

The international team recognized the impact of the epidemic on Wuhan, from affected individuals and communities to government officials, scientists and health workers. The team commended the engagement of all the professionals who had spent long hours analysing very large quantities of data to support its work. In conclusion, the team called for a continued scientific and collaborative approach to be taken towards tracing the origins of COVID-19.

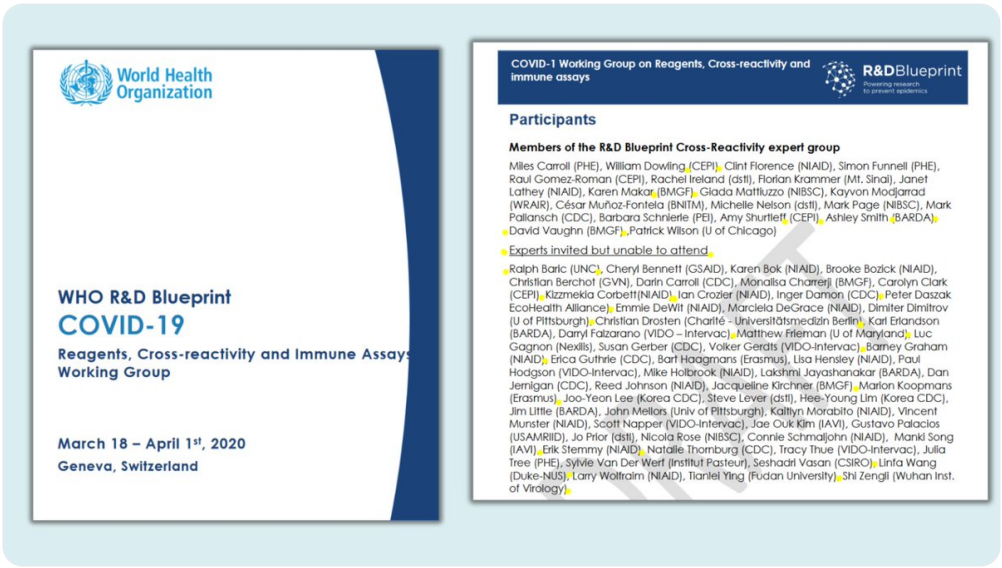
References

(1) Likert R. (1932). A technique for the measurement of attitudes. Archives of Psychology, 140:44–53.

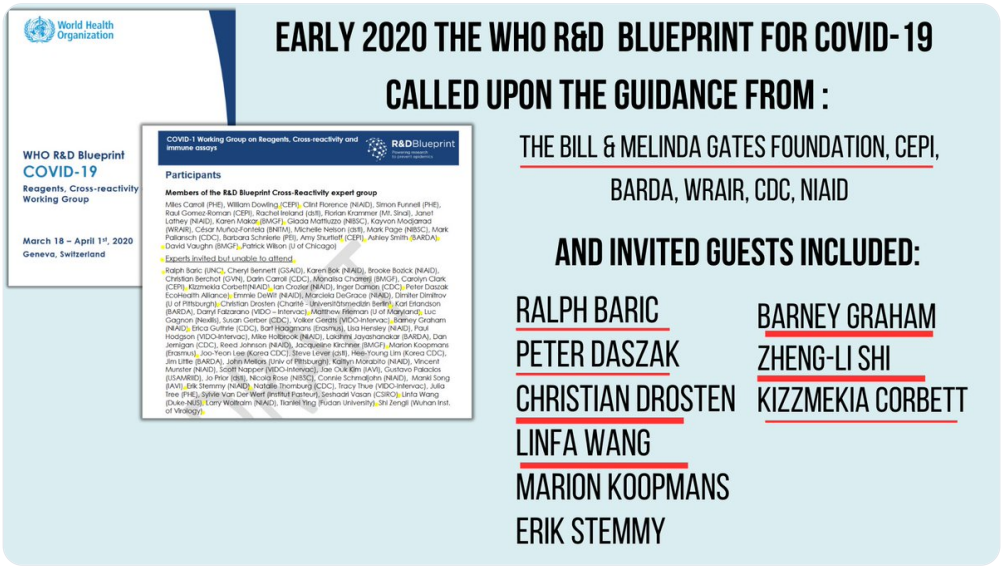
(2) Olival, K., Hosseini, P., Zambrana-Torrelio, C. et al. Host and viral traits predict zoonotic spillover from mammals. Nature 546, 646–650 (2017)

(3) Andersen KG, Rambaut A, Lipkin WI, Holmes EC, and Garry RF (2020). The proximal origin of SARS-CoV-2. Nature Medicine 26:450-452

13🧵What about the WHO R&D Blueprint for C19 working group report from March 2020? Tasked w/ setting the standards for immune assays from viral samples for gov guidance. Help from Bill Gates, CEPI, BARDA & the CDC means they surely had a impartial member committee. ...Right?


World Health Organization
WHO R&D Blueprint
COVID-19
Reagents, Cross-reactivity and Immune Assays Working Group
March 18 – April 1st, 2020
Geneva, Switzerland
COVID-1 Working Group on Reagents, Cross-reactivity and immune assays
R&DBlueprint
Participants
Members of the R&D Blueprint Cross-Reactivity expert group
Miles Carroll (PHE), William Dowling (CEPI), Clint Florence (NIAID), Simon Funnell (PHE), Raul Gomez-Roman (CEPI), Rachel Ireland (dstl), Florian Krammer (Mt. Sinai), Janet Lathey (NIAID), Karen Makar (BMGF), Gisela Mattiuzzo (NIBSC), Kayvon Modjarrad (WRAIR), César Muñoz-Fontela (BNITM), Michelle Nelson (dstl), Mark Page (NIBSC), Mark Pallansch (CDC), Barbara Schnierle (PEI), Amy Shurtleff (CEPI), Ashley Smith (BARDA), David Vaughn (BMGF), Patrick Wilson (U of Chicago)
Experts invited but unable to attend
Ralph Baric (UNC), Cheryl Bennett (GSAID), Karen Bok (NIAID), Brooke Bozick (NIAID), Christian Berchot (GVN), Darin Carroll (CDC), Monalisa Charreji (BMGF), Carolyn Clark (CEPI), Kizzmekia Corbett(NIAID), Ian Crozier (NIAID), Inger Damon (CDC), Peter Daszak EcoHealth Alliance), Emmie DeWit (NIAID), Marciela DeGrace (NIAID), Dimiter Dimitrov (U of Pittsburgh), Christian Drosten (Charité - Universitätsmedizin Berlin), Karl Erlandson (BARDA), Darryl Falzarano (VIDO – Intervac), Matthew Frieman (U of Maryland), Luc Gagnon (Nexilis), Susan Gerber (CDC), Volker Gerdts (VIDO-Intervac), Barney Graham (NIAID), Erica Guthrie (CDC), Bart Haagmans (Erasmus), Lisa Hensley (NIAID), Paul Hodgson (VIDO-Intervac), Mike Holbrook (NIAID), Lakshmi Jayashanakar (BARDA), Dan Jernigan (CDC), Reed Johnson (NIAID), Jacqueline Kirchner (BMGF), Marion Koopmans (Erasmus), Joo-Yeon Lee (Korea CDC), Steve Lever (dstl), Hee-Young Lim (Korea CDC), Jim Little (BARDA), John Mellors (Univ of Pittsburgh), Kaitlyn Morabito (NIAID), Vincent Munster (NIAID), Scott Napper (VIDO-Intervac), Jae Ouk Kim (IAVI), Gustavo Palacios (USAMRIID), Jo Prior (dstl), Nicola Rose (NIBSC), Connie Schmaljohn (NIAID), Manki Song (IAVI), Erik Stemmy (NIAID), Natalie Thornburg (CDC), Tracy Thue (VIDO-Intervac), Julia Tree (PHE), Sylvie Van Der Werf (Institut Pasteur), Seshadri Vasan (CSIRO), Linfa Wang (Duke-NUS), Larry Wolfraim (NIAID), Tianlei Ying (Fudan University), Shi Zengli (Wuhan Inst. of Virology).

14🧵WRONG. Dead wrong.🚫 The Invited guest included: Ralph Baric, Peter Daszak, Christian Drosten, Linfa Wang, Koopmans, Stemmy, Zhengli Shi, Barney Graham & Kizzmekia Corbett. So the GoF scientists, & the NIH scientists credited w/ creating the C19 vaccine.🤦‍♀️



🧾Receipts:

https://www.who.int/docs/default-source/coronaviruse/rd-blueprint-lab-expert-group-cross-reactivity-call-18-mar-1-apr-2020.pdf

WHO-convened Global Study of Origins of SARS-CoV-2: China Part | J…
Analysis in English on World and 1 other country about Health and Epidemic; published on 30 Mar 2021 by WHO

https://reliefweb.int/report/world/who-convened-global-study-origins-sars-cov-2-china-p…

My Sources?

https://usrtk.org/wp-content/uploads/2021/04/Saif-OSU-Batch-1.pdf
https://usrtk.org/wp-content/uploads/2022/12/UNC_Daszak-Media-Story.pdf
https://www.biorxiv.org/content/10.1101/768663v1.full.pdf
https://reliefweb.int/report/world/who-convened-global-study-origins-sars-cov-2-china-part-joint-who-china-study-14
https://www.who.int/publications/m/item/who-convened-global-study-of-the-origins-of-sars-cov-2
https://covid19.who.int/ https://ori.hhs.gov/education/products/ucla/chapter4/default.html
https://reporter.nih.gov/search/qkWL0AV0pUC-ztQD6umk-A/project-details/9328799 https://grantome.com/search?q=R01AI110700 https://www.nature.com/articles/s41579-018-0118-9
https://grantome.com/search?q=AI089728 https://pubmed.ncbi.nlm.nih.gov/27578435/
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf
https://reporter.nih.gov/search/qkWL0AV0pUC-ztQD6umk-A/project-details/9328799
https://pubmed.ncbi.nlm.nih.gov/28807998/ https://grantome.com/grant/NIH/R01-AI127521-01A1
https://patents.justia.com/patent/20200061185#history
https://www.scripps.edu/_files/pdfs/campuses/florida/annualreport2020.pdf
https://cdr.lib.unc.edu/downloads/zs25xd890 https://etd.ohiolink.edu/acprod/odb_etd/ws/send_file/send?accession=osu1681753185391367&disposition=inline
https://www.biorxiv.org/content/10.1101/768663v1.full.pdf https://www.science.org/doi/10.1126/scitranslmed.aal3653
https://journals.asm.org/doi/10.1128/jvi.03079-15
https://usrtk.org/wp-content/uploads/2022/12/UNC_Daszak-Media-Story.pdf
https://twitter.com/COVIDSelect/status/1730692429051826435

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